

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gallatin, W. Michael
Kilgannon, Patrick D.
- (ii) TITLE OF INVENTION: ICAM-4 Materials and Methods
- (iii) NUMBER OF SEQUENCES: 42
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/827,689
 - (B) FILING DATE: 27-JAN-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/889,724
 - (B) FILING DATE: 26-MAY-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/894,061
 - (B) FILING DATE: 05-JUN-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/009,266
 - (B) FILING DATE: 22-JAN-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/102,852
 - (B) FILING DATE: 05-AUG-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/245,295
 - (B) FILING DATE: 18-MAY-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/485,604
 - (B) FILING DATE: 07-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: WILLIAMS, JR. JOSEPH A.
 - (B) REGISTRATION NUMBER: 38,659
 - (C) REFERENCE/DOCKET NUMBER: 27866/33321

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2988 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 61..2814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATTGATCA CTCGCGCTCC CCTCGCCCTTC TGCGCTCTCC CCTCCCTGGC AGCGGCCGGCA	60
ATG CCG GGG CCT TCA CCA GGG CTG CGC CGA ACG CTC CTC GGC CTC TGG Met Pro Gly Pro Ser Pro Gly Leu Arg Arg Thr Leu Leu Gly Leu Trp	108
1 5 10 15	
GCT GCC CTG GGC CTG GGG ATC CTA GGC ATC TCA GCG GTC GCG CTA GAA Ala Ala Leu Gly Leu Gly Ile Leu Gly Ile Ser Ala Val Ala Leu Glu	156
20 25 30	
CCT TTC TGG GCG GAC CTT CAG CCC CGC GTG GCG CTC GTG GAG CGC GGG Pro Phe Trp Ala Asp Leu Gln Pro Arg Val Ala Leu Val Glu Arg Gly	204
35 40 45	
GGC TCG CTG TGG CTC AAC TGC AGC ACT AAC TGT CCG AGG CCG GAG CGC Gly Ser Leu Trp Leu Asn Cys Ser Thr Asn Cys Pro Arg Pro Glu Arg	252
50 55 60	
GGT GGC CTG GAG ACC TCG CTA CGC CGA AAC GGG ACC CAG AGG GGT CTG Gly Gly Leu Glu Thr Ser Leu Arg Arg Asn Gly Thr Gln Arg Gly Leu	300
65 70 75 80	
CGC TGG CTG GCT CGA CAG CTG GTG GAC ATC CGA GAG CCT GAA ACC CAG Arg Trp Leu Ala Arg Gln Leu Val Asp Ile Arg Glu Pro Glu Thr Gln	348
85 90 95	
CCG GTC TGC TTC CGC TGC GCG CGC CGC ACA CTC CAA GCG CGT GGG Pro Val Cys Phe Phe Arg Cys Ala Arg Arg Thr Leu Gln Ala Arg Gly	396
100 105 110	
CTC ATC CGA ACT TTC CAG CGA CCG GAT CGG GTA GAG CTA GTG CCT CTG Leu Ile Arg Thr Phe Gln Arg Pro Asp Arg Val Glu Leu Val Pro Leu	444
115 120 125	
CCT CCT TGG CAG CCT GTA GGT GAG AAC TTC ACC TTG AGC TGC AGG GTC Pro Pro Trp Gln Pro Val Gly Glu Asn Phe Thr Leu Ser Cys Arg Val	492
130 135 140	
CCG GGG GCA GGA CCC CGA GCG AGC CTC ACA TTG ACC TTG CTG CGA GGC Pro Gly Ala Gly Pro Arg Ala Ser Leu Thr Leu Thr Leu Leu Arg Gly	540
145 150 155 160	

GGC CAG GAG CTG ATT CGC CGA AGT TTC GTA GGC GAG CCA CCC CGA GCT Gly Gln Glu Leu Ile Arg Arg Ser Phe Val Gly Glu Pro Pro Arg Ala 165 170 175	588
CGG GGT GCG ATG CTC ACC GCC ACG GTC CTG GCG CGC AGA GAG GAT CAC Arg Gly Ala Met Leu Thr Ala Thr Val Leu Ala Arg Arg Glu Asp His 180 185 190	636
AGG GCC AAT TTC TCA TGC CTC GCG GAG CTT GAC CTG CGG CCA CAC GGC Arg Ala Asn Phe Ser Cys Leu Ala Glu Leu Asp Leu Arg Pro His Gly 195 200 205	684
TTG GGA CTG TTT GCA AAC AGC TCA GCC CCC AGA CAG CTC CGC ACG TTT Leu Gly Leu Phe Ala Asn Ser Ser Ala Pro Arg Gln Leu Arg Thr Phe 210 215 220	732
GCC ATG CCT CCA CTT TCC CCG AGC CTT ATT GCC CCA CGA TTC TTA GAA Ala Met Pro Pro Leu Ser Pro Ser Leu Ile Ala Pro Arg Phe Leu Glu 225 230 235 240	780
GTG GGC TCA GAA AGG CCG GTG ACT TGC ACT TTG GAT GGA CTG TTT CCT Val Gly Ser Glu Arg Pro Val Thr Cys Thr Leu Asp Gly Leu Phe Pro 245 250 255	828
GCC CCA GAA GCC GGG GTT TAC CTC TCT CTG GGA GAT CAG AGG CTT CAT Ala Pro Glu Ala Gly Val Tyr Leu Ser Leu Gly Asp Gln Arg Leu His 260 265 270	876
CCT AAT GTG ACC CTC GAC GGG GAG AGC CTT GTG GCC ACT GCC ACA GCT Pro Asn Val Thr Leu Asp Gly Glu Ser Leu Val Ala Thr Ala Thr Ala 275 280 285	924
ACA GCA AGT GAA GAA CAG GAA GGC ACC AAA CAG CTG ATG TGC ATC GTG Thr Ala Ser Glu Glu Gln Glu Gly Thr Lys Gln Leu Met Cys Ile Val 290 295 300	972
ACC CTC GGG GGC GAA AGC AGG GAG ACC CAG GAA AAC CTG ACT GTC TAC Thr Leu Gly Gly Glu Ser Arg Glu Thr Gln Glu Asn Leu Thr Val Tyr 305 310 315 320	1020
AGC TTC CCG GCT CCT CTT CTG ACT TTA AGT GAG CCA GAA GCC CCC GAG Ser Phe Pro Ala Pro Leu Leu Thr Leu Ser Glu Pro Glu Ala Pro Glu 325 330 335	1068
GGA AAG ATG GTG ACC GTA AGC TGC TGG GCA GGG GCC CGA GCC CTT GTC Gly Lys Met Val Thr Val Ser Cys Trp Ala Gly Ala Arg Ala Leu Val 340 345 350	1116
ACC TTG GAG GGA ATT CCA GCT GCG GTC CCT GGG CAG CCC GCT GAG CTC Thr Leu Glu Gly Ile Pro Ala Ala Val Pro Gly Gln Pro Ala Glu Leu 355 360 365	1164
CAG TTA AAT GTC ACA AAG AAT GAC GAC AAG CGG GGC TTC TTC TGC GAC Gln Leu Asn Val Thr Lys Asn Asp Asp Lys Arg Gly Phe Phe Cys Asp 370 375 380	1212
GCT GCC CTC GAT GTG GAC GGG GAA ACT CTG AGA AAG AAC CAG AGC TCT Ala Ala Leu Asp Val Asp Gly Glu Thr Leu Arg Lys Asn Gln Ser Ser 385 390 395 400	1260
GAG CTT CGT GTT CTG TAC GCA CCT CGG CTG GAT GAC TTG GAC TGT CCC Glu Leu Arg Val Leu Tyr Ala Pro Arg Leu Asp Asp Leu Asp Cys Pro 405 410 415	1308

AGG AGC TGG ACG TGG CCA GAG GGT CCA GAG CAG ACC CTC CAC TGC GAG Arg Ser Trp Thr Trp Pro Glu Gly Pro Glu Gln Thr Leu His Cys Glu 420 425 430	1356
GCC CGT GGA AAC CCT GAG CCC TCC GTG CAC TGT GCA AGG CCT GAC GGT Ala Arg Gly Asn Pro Glu Pro Ser Val His Cys Ala Arg Pro Asp Gly 435 440 445	1404
GGG GCG GTG CTA GCG CTG GGC CTG TTG GGT CCA GTG ACC CGT GCC CTC Gly Ala Val Leu Ala Leu Gly Leu Leu Gly Pro Val Thr Arg Ala Leu 450 455 460	1452
GCG GGC ACT TAC CGA TGT ACA GCA ATC AAT GGG CAA GGC CAG GCG GTC Ala Gly Thr Tyr Arg Cys Thr Ala Ile Asn Gly Gln Gly Gln Ala Val 465 470 475 480	1500
AAG GAT GTG ACC CTG ACT GTG GAA TAT GCC CCA GCG CTG GAC AGT GTA Lys Asp Val Thr Leu Thr Val Glu Tyr Ala Pro Ala Leu Asp Ser Val 485 490 495	1548
GGC TGC CCA GAA CGT ATT ACT TGG CTG GAG GGG ACA GAG GCA TCG CTT Gly Cys Pro Glu Arg Ile Thr Trp Leu Glu Gly Thr Glu Ala Ser Leu 500 505 510	1596
AGC TGT GTG GCA CAC GGG GTC CCA CCA CCT AGC GTG AGC TGT GTG CGC Ser Cys Val Ala His Gly Val Pro Pro Pro Ser Val Ser Cys Val Arg 515 520 525	1644
TCT GGA AAG GAG GAA GTC ATG GAA GGG CCC CTG CGT GTG GCC CGG GAG Ser Gly Lys Glu Glu Val Met Glu Gly Pro Leu Arg Val Ala Arg Glu 530 535 540	1692
CAC GCT GGC ACT TAC CGA TGC GAA GCC ATC AAC GCC AGG GGA TCA GCG His Ala Gly Thr Tyr Arg Cys Glu Ala Ile Asn Ala Arg Gly Ser Ala 545 550 555 560	1740
GCC AAA AAT GTG GCT GTC ACG GTG GAA TAT GGT CCC AGT TTT GAG GAG Ala Lys Asn Val Ala Val Thr Val Glu Tyr Gly Pro Ser Phe Glu Glu 565 570 575	1788
TTG GGC TGC CCC AGC AAC TGG ACT TGG GTA GAA GGA TCT GGA AAA CTG Leu Gly Cys Pro Ser Asn Trp Thr Trp Val Glu Gly Ser Gly Lys Leu 580 585 590	1836
TTT TCC TGT GAA GTT GAT GGG AAG CCG GAA CCA CGC GTG GAG TGC GTG Phe Ser Cys Glu Val Asp Gly Lys Pro Glu Pro Arg Val Glu Cys Val 595 600 605	1884
GGC TCG GAG GGT GCA AGC GAA GGG GTA GTG TTG CCC CTG GTG TCC TCG Gly Ser Glu Gly Ala Ser Glu Gly Val Val Leu Pro Leu Val Ser Ser 610 615 620	1932
AAC TCT GGT TCC AGA AAC TCT ATG ACT CCT GGT AAC CTG TCA CCG GGT Asn Ser Gly Ser Arg Asn Ser Met Thr Pro Gly Asn Leu Ser Pro Gly 625 630 635 640	1980
ATT TAC CTC TGC AAC GCC ACC AAC CGG CAT GGC TCC ACA GTC AAA ACA Ile Tyr Leu Cys Asn Ala Thr Asn Arg His Gly Ser Thr Val Lys Thr 645 650 655	2028
GTC GTC GTG AGC GCG GAA TCA CCG CCA CAG ATG GAT GAA TCC AGT TGC Val Val Val Ser Ala Glu Ser Pro Pro Gln Met Asp Glu Ser Ser Cys 660 665 670	2076

CCG AGT CAC CAG ACA TGG CTG GAA GGA GCC GAG GCT ACT GCG CTG GCC Pro Ser His Gln Thr Trp Leu Glu Gly Ala Glu Ala Thr Ala Leu Ala 675 680 685	2124
TGC AGT GCC AGA GGC CGC CCC TCT CCA CGC GTG CGC TGT TCC AGG GAA Cys Ser Ala Arg Gly Arg Pro Ser Pro Arg Val Arg Cys Ser Arg Glu 690 695 700	2172
GGT GCA GCC AGG CTG GAG AGG CTA CAG GTG TCC CGA GAG GAT GCG GGG Gly Ala Ala Arg Leu Glu Arg Leu Gln Val Ser Arg Glu Asp Ala Gly 705 710 715 720	2220
ACC TAC CTG TGT GTG GCT ACC AAC GCG CAT GGC ACG GAT TCA CGG ACC Thr Tyr Leu Cys Val Ala Thr Asn Ala His Gly Thr Asp Ser Arg Thr 725 730 735	2268
GTC ACT GTG GGT GTG GAA TAC CGG CCT GTG GTG GCT GAG CTG GCA GCC Val Thr Val Gly Val Glu Tyr Arg Pro Val Val Ala Glu Leu Ala Ala 740 745 750	2316
TCG CCC CCA AGC GTG CGG CCT GGC GGA AAC TTC ACT CTG ACC TGC CGT Ser Pro Pro Ser Val Arg Pro Gly Gly Asn Phe Thr Leu Thr Cys Arg 755 760 765	2364
GCA GAG GCC TGG CCT CCA GCC CAG ATC AGC TGG CGC GCG CCC CCG GGA Ala Glu Ala Trp Pro Pro Ala Gln Ile Ser Trp Arg Ala Pro Pro Gly 770 775 780	2412
GCT CTC AAC CTC GGT CTC TCC AGC AAC AAC AGC ACG CTG AGC GTG GCG Ala Leu Asn Leu Gly Leu Ser Ser Asn Asn Ser Thr Leu Ser Val Ala 785 790 795 800	2460
GGT GCC ATG GGC AGC CAT GGT GGC GAG TAT GAG TGC GCA GCC ACC AAT Gly Ala Met Gly Ser His Gly Gly Glu Tyr Glu Cys Ala Ala Thr Asn 805 810 815	2508
GCG CAT GGG CGC CAC GCA CGG CGC ATC ACG GTG CGC GTG GCC GGT CCA Ala His Gly Arg His Ala Arg Arg Ile Thr Val Arg Val Ala Gly Pro 820 825 830	2556
TGG CTG TGG GTC GCT GTG GGC GGT GCG GCA GGG GGC GCG GCG CTG CTG Trp Leu Trp Val Ala Val Gly Gly Ala Ala Gly Gly Ala Ala Leu Leu 835 840 845	2604
GCC GCA GGG GCC GGC CTG GCC TTC TAC GTG CAG TCC ACC GCT TGC AAG Ala Ala Gly Ala Gly Leu Ala Phe Tyr Val Gln Ser Thr Ala Cys Lys 850 855 860	2652
AAG GGA GAG TAC AAC GTC CAG GAG GCT GAG AGC TCA GGC GAG GCG GTG Lys Gly Glu Tyr Asn Val Gln Glu Ala Glu Ser Ser Gly Glu Ala Val 865 870 875 880	2700
TGT CTC AAT GGC GCG GGC GGG ACA CCG GGT GCA GAA GGC GGA GCA GAG Cys Leu Asn Gly Ala Gly Gly Thr Pro Gly Ala Glu Gly Gly Ala Glu 885 890 895	2748
ACC CCC GGC ACT GCC GAG TCA CCT GCA GAT GGC GAG GTT TTC GCC ATC Thr Pro Gly Thr Ala Glu Ser Pro Ala Asp Gly Glu Val Phe Ala Ile 900 905 910	2796
CAG CTG ACA TCT TCC TGAGCCTGTA TCCAGCTCCC CCAGGGGCCT CGAAAGCACA Gln Leu Thr Ser Ser 915	2851

GGGGTGGACG TATGTATTGT TCACTCTCTA TTTATTCAAC TCCAGGGGCG TCGTCCCCGT	2911
TTTCTACCCA TTCCCTTAAT AAAGTTTTA TAGGAGAAAA AAAAAAAAAA AAAAAAAAAA	2971
AAAAAAAAAA AAAAAAAA	2988

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 917 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Gly Pro Ser Pro Gly Leu Arg Arg Thr Leu Leu Gly Leu Trp	
1 5 10 15	
Ala Ala Leu Gly Leu Gly Ile Leu Gly Ile Ser Ala Val Ala Leu Glu	
20 25 30	
Pro Phe Trp Ala Asp Leu Gln Pro Arg Val Ala Leu Val Glu Arg Gly	
35 40 45	
Gly Ser Leu Trp Leu Asn Cys Ser Thr Asn Cys Pro Arg Pro Glu Arg	
50 55 60	
Gly Gly Leu Glu Thr Ser Leu Arg Arg Asn Gly Thr Gln Arg Gly Leu	
65 70 75 80	
Arg Trp Leu Ala Arg Gln Leu Val Asp Ile Arg Glu Pro Glu Thr Gln	
85 90 95	
Pro Val Cys Phe Phe Arg Cys Ala Arg Arg Thr Leu Gln Ala Arg Gly	
100 105 110	
Leu Ile Arg Thr Phe Gln Arg Pro Asp Arg Val Glu Leu Val Pro Leu	
115 120 125	
Pro Pro Trp Gln Pro Val Gly Glu Asn Phe Thr Leu Ser Cys Arg Val	
130 135 140	
Pro Gly Ala Gly Pro Arg Ala Ser Leu Thr Leu Thr Leu Leu Arg Gly	
145 150 155 160	
Gly Gln Glu Leu Ile Arg Arg Ser Phe Val Gly Glu Pro Pro Arg Ala	
165 170 175	
Arg Gly Ala Met Leu Thr Ala Thr Val Leu Ala Arg Arg Glu Asp His	
180 185 190	
Arg Ala Asn Phe Ser Cys Leu Ala Glu Leu Asp Leu Arg Pro His Gly	
195 200 205	
Leu Gly Leu Phe Ala Asn Ser Ser Ala Pro Arg Gln Leu Arg Thr Phe	
210 215 220	
Ala Met Pro Pro Leu Ser Pro Ser Leu Ile Ala Pro Arg Phe Leu Glu	
225 230 235 240	

Val Gly Ser Glu Arg Pro Val Thr Cys Thr Leu Asp Gly Leu Phe Pro
245 250 255

Ala Pro Glu Ala Gly Val Tyr Leu Ser Leu Gly Asp Gln Arg Leu His
260 265 270

Pro Asn Val Thr Leu Asp Gly Glu Ser Leu Val Ala Thr Ala Thr Ala
275 280 285

Thr Ala Ser Glu Glu Gln Gly Thr Lys Gln Leu Met Cys Ile Val
290 295 300

Thr Leu Gly Gly Glu Ser Arg Glu Thr Gln Glu Asn Leu Thr Val Tyr
305 310 315 320

Ser Phe Pro Ala Pro Leu Leu Thr Leu Ser Glu Pro Glu Ala Pro Glu
325 330 335

Gly Lys Met Val Thr Val Ser Cys Trp Ala Gly Ala Arg Ala Leu Val
340 345 350

Thr Leu Glu Gly Ile Pro Ala Ala Val Pro Gly Gln Pro Ala Glu Leu
355 360 365

Gln Leu Asn Val Thr Lys Asn Asp Asp Lys Arg Gly Phe Phe Cys Asp
370 375 380

Ala Ala Leu Asp Val Asp Gly Glu Thr Leu Arg Lys Asn Gln Ser Ser
385 390 395 400

Glu Leu Arg Val Leu Tyr Ala Pro Arg Leu Asp Asp Leu Asp Cys Pro
405 410 415

Arg Ser Trp Thr Trp Pro Glu Gly Pro Glu Gln Thr Leu His Cys Glu
420 425 430

Ala Arg Gly Asn Pro Glu Pro Ser Val His Cys Ala Arg Pro Asp Gly
435 440 445

Gly Ala Val Leu Ala Leu Gly Leu Leu Gly Pro Val Thr Arg Ala Leu
450 455 460

Ala Gly Thr Tyr Arg Cys Thr Ala Ile Asn Gly Gln Gly Gln Ala Val
465 470 475 480

Lys Asp Val Thr Leu Thr Val Glu Tyr Ala Pro Ala Leu Asp Ser Val
485 490 495

Gly Cys Pro Glu Arg Ile Thr Trp Leu Glu Gly Thr Glu Ala Ser Leu
500 505 510

Ser Cys Val Ala His Gly Val Pro Pro Pro Ser Val Ser Cys Val Arg
515 520 525

Ser Gly Lys Glu Glu Val Met Glu Gly Pro Leu Arg Val Ala Arg Glu
530 535 540

His Ala Gly Thr Tyr Arg Cys Glu Ala Ile Asn Ala Arg Gly Ser Ala
545 550 555 560

Ala Lys Asn Val Ala Val Thr Val Glu Tyr Gly Pro Ser Phe Glu Glu
565 570 575

Leu Gly Cys Pro Ser Asn Trp Thr Trp Val Glu Gly Ser Gly Lys Leu
580 585 590

Phe Ser Cys Glu Val Asp Gly Lys Pro Glu Pro Arg Val Glu Cys Val
595 600 605

Gly Ser Glu Gly Ala Ser Glu Gly Val Val Leu Pro Leu Val Ser Ser
610 615 620

Asn Ser Gly Ser Arg Asn Ser Met Thr Pro Gly Asn Leu Ser Pro Gly
625 630 635 640

Ile Tyr Leu Cys Asn Ala Thr Asn Arg His Gly Ser Thr Val Lys Thr
645 650 655

Val Val Val Ser Ala Glu Ser Pro Pro Gln Met Asp Glu Ser Ser Cys
660 665 670

Pro Ser His Gln Thr Trp Leu Glu Gly Ala Glu Ala Thr Ala Leu Ala
675 680 685

Cys Ser Ala Arg Gly Arg Pro Ser Pro Arg Val Arg Cys Ser Arg Glu
690 695 700

Gly Ala Ala Arg Leu Glu Arg Leu Gln Val Ser Arg Glu Asp Ala Gly
705 710 715 720

Thr Tyr Leu Cys Val Ala Thr Asn Ala His Gly Thr Asp Ser Arg Thr
725 730 735

Val Thr Val Gly Val Glu Tyr Arg Pro Val Val Ala Glu Leu Ala Ala
740 745 750

Ser Pro Pro Ser Val Arg Pro Gly Gly Asn Phe Thr Leu Thr Cys Arg
755 760 765

Ala Glu Ala Trp Pro Pro Ala Gln Ile Ser Trp Arg Ala Pro Pro Gly
770 775 780

Ala Leu Asn Leu Gly Leu Ser Ser Asn Asn Ser Thr Leu Ser Val Ala
785 790 795 800

Gly Ala Met Gly Ser His Gly Gly Glu Tyr Glu Cys Ala Ala Thr Asn
805 810 815

Ala His Gly Arg His Ala Arg Arg Ile Thr Val Arg Val Ala Gly Pro
820 825 830

Trp Leu Trp Val Ala Val Gly Gly Ala Ala Gly Gly Ala Ala Leu Leu
835 840 845

Ala Ala Gly Ala Gly Leu Ala Phe Tyr Val Gln Ser Thr Ala Cys Lys
850 855 860

Lys Gly Glu Tyr Asn Val Gln Glu Ala Glu Ser Ser Gly Glu Ala Val
865 870 875 880

Cys Leu Asn Gly Ala Gly Gly Thr Pro Gly Ala Glu Gly Gly Ala Glu
885 890 895

Thr Pro Gly Thr Ala Glu Ser Pro Ala Asp Gly Glu Val Phe Ala Ile
900 905 910

Gln Leu Thr Ser Ser
915

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCG GAT CGG GTA GAG CTA GTG CCT CTG CCT CCT TGG CAG CCT GTA GGT	48
Pro Asp Arg Val Glu Leu Val Pro Leu Pro Pro Trp Gln Pro Val Gly	
1 5 10 15	
GAG AAC TTC ACC TTG AGC TGC AGG GTC CCG GGG GCA GGA CCC CGA GCG	96
Glu Asn Phe Thr Leu Ser Cys Arg Val Pro Gly Ala Gly Pro Arg Ala	
20 25 30	
AGC CTC ACA TTG ACC TTG CTG CGA GGC GGA CAG GAG CTG ATT CGC CGA	144
Ser Leu Thr Leu Leu Arg Gly Gly Gln Glu Leu Ile Arg Arg	
35 40 45	
AGT TTC GTA GGC GAG CCA CCC CGA GCT CGG TGT GCG ATG CTC ACC GCC	192
Ser Phe Val Gly Glu Pro Pro Arg Ala Arg Cys Ala Met Leu Thr Ala	
50 55 60	
ACG GTC CTG GCG CGC AGA GAG GAT CAC AGG GAC AAT TTC TCA TGC CTC	240
Thr Val Leu Ala Arg Arg Glu Asp His Arg Asp Asn Phe Ser Cys Leu	
65 70 75 80	
GCG GAG CTT GAC CTG CGG ACA CAC GGC TTG GGA CTG TTT GCA AAC AGC	288
Ala Glu Leu Asp Leu Arg Thr His Gly Leu Gly Leu Phe Ala Asn Ser	
85 90 95	
TCA GCC CCC AGA CAG CTC CGC ACG TTT	315
Ser Ala Pro Arg Gln Leu Arg Thr Phe	
100 105	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1781 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 16..1659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGCTCTCTG TCAGA ATG GCC ACC ATG GTA CCA TCC GTG TTG TGG CCC AGG Met Ala Thr Met Val Pro Ser Val Leu Trp Pro Arg 1 5 10	51
GCC TGC TGG ACT CTG CTG GTC TGC TGT CTG CTG ACC CCA GGT GTC CAG Ala Cys Trp Thr Leu Leu Val Cys Cys Leu Leu Thr Pro Gly Val Gln 15 20 25	99
GGG CAG GAG TTC CTT TTG CGG GTG GAG CCC CAG AAC CCT GTG CTC TCT Gly Gln Glu Phe Leu Leu Arg Val Glu Pro Gln Asn Pro Val Leu Ser 30 35 40	147
GCT GGA GGG TCC CTG TTT GTG AAC TGC AGT ACT GAT TGT CCC AGC TCT Ala Gly Gly Ser Leu Phe Val Asn Cys Ser Thr Asp Cys Pro Ser Ser 45 50 55 60	195
GAG AAA ATC GCC TTG GAG ACG TCC CTA TCA AAG GAG CTG GTG GCC AGT Glu Lys Ile Ala Leu Glu Thr Ser Leu Ser Lys Glu Leu Val Ala Ser 65 70 75	243
GGC ATG GGC TGG GCA GCC TTC AAT CTC AGC AAC GTG ACT GGC AAC AGT Gly Met Gly Trp Ala Ala Phe Asn Leu Ser Asn Val Thr Gly Asn Ser 80 85 90	291
CGG ATC CTC TGC TCA GTG TAC TGC AAT GGC TCC CAG ATA ACA GGC TCC Arg Ile Leu Cys Ser Val Tyr Cys Asn Gly Ser Gln Ile Thr Gly Ser 95 100 105	339
TCT AAC ATC ACC GTG TAC GGG CTC CCG GAG CGT GTG GAG CTG GCA CCC Ser Asn Ile Thr Val Tyr Gly Leu Pro Glu Arg Val Glu Leu Ala Pro 110 115 120	387
CTG CCT CCT TGG CAG CCG GTG GGC CAG AAC TTC ACC CTG CGC TGC CAA Leu Pro Pro Trp Gln Pro Val Gly Gln Asn Phe Thr Leu Arg Cys Gln 125 130 135 140	435
GTG GAG GGT GGG TCG CCC CGG ACC AGC CTC ACG GTG GTG CTG CTT CGC Val Glu Gly Ser Pro Arg Thr Ser Leu Thr Val Val Leu Leu Arg 145 150 155	483
TGG GAG GAG GAG CTG AGC CGG CAG CCC GCA GTG GAG GAG CCA GCG GAG Trp Glu Glu Glu Leu Ser Arg Gln Pro Ala Val Glu Glu Pro Ala Glu 160 165 170	531
GTC ACT GCC ACT GTG CTG GCC AGC AGA GAC GAC CAC GGA GCC CCT TTC Val Thr Ala Thr Val Leu Ala Ser Arg Asp Asp His Gly Ala Pro Phe 175 180 185	579
TCA TGC CGC ACA GAA CTG GAC ATG CAG CCC CAG GGG CTG GGA CTG TTC Ser Cys Arg Thr Glu Leu Asp Met Gln Pro Gln Gly Leu Gly Leu Phe 190 195 200	627
GTG AAC ACC TCA GCC CCC CGC CAG CTC CGA ACC TTT GTC CTG CCC GTG Val Asn Thr Ser Ala Pro Arg Gln Leu Arg Thr Phe Val Leu Pro Val 205 210 215 220	675
ACC CCC CCG CGC CTC GTG GCC CCC CGG TTC TTG GAG GTG GAA ACG TCG Thr Pro Pro Arg Leu Val Ala Pro Arg Phe Leu Glu Val Glu Thr Ser 225 230 235	723
TGG CCG GTG GAC TGC ACC CTA GAC GGG CTT TTT CCA GCC TCA GAG GCC Trp Pro Val Asp Cys Thr Leu Asp Gly Leu Phe Pro Ala Ser Glu Ala 240 245 250	771

CAG GTC TAC CTG GCG CTG GGG GAC CAG ATG CTG AAT GCG ACA GTC ATG Gln Val Tyr Leu Ala Leu Gly Asp Gln Met Leu Asn Ala Thr Val Met 255 260 265	819
AAC CAC GGG GAC ACG CTA ACG GCC ACA GCC ACA GCG ACC GCG CGC GCG Asn His Gly Asp Thr Leu Thr Ala Thr Ala Thr Ala Arg Ala 270 275 280	867
GAT CAG GAG GGT GCC CGG GAG ATC GTC TGC AAC GTG ACC CTA GGG GGC Asp Gln Glu Gly Ala Arg Glu Ile Val Cys Asn Val Thr Leu Gly Gly 285 290 295 300	915
GAG AGA CGG GAG GCC CGG GAG AAC TTG ACG GTC TTT AGC TTC CTA GGA Glu Arg Arg Glu Ala Arg Glu Asn Leu Thr Val Phe Ser Phe Leu Gly 305 310 315	963
CCC ATT GTG AAC CTC AGC GAG CCC ACC GCC CAT GAG GGG TCC ACA GTG Pro Ile Val Asn Leu Ser Glu Pro Thr Ala His Glu Gly Ser Thr Val 320 325 330	1011
ACC GTG AGT TGC ATG GCT GGG GCT CGA GTC CAG GTC ACG CTG GAC GGA Thr Val Ser Cys Met Ala Gly Ala Arg Val Gln Val Thr Leu Asp Gly 335 340 345	1059
GTT CCG GCC GCG GCC CCG GGG CAG ACA GCT CAA CTT CAG CTA AAT GCT Val Pro Ala Ala Ala Pro Gly Gln Thr Ala Gln Leu Gln Leu Asn Ala 350 355 360	1107
ACC GAG AGT GAC GAC GGA CGC AGC TTC TTC TGC AGT GCC ACT CTC GAG Thr Glu Ser Asp Asp Gly Arg Ser Phe Phe Cys Ser Ala Thr Leu Glu 365 370 375 380	1155
GTG GAC GGC GAG TTC TTG CAC AGG AAC AGT AGC GTC CAG CTG CGA GTC Val Asp Gly Glu Phe Leu His Arg Asn Ser Ser Val Gln Leu Arg Val 385 390 395	1203
CTG TAT GGT CCC AAA ATT GAC CGA GCC ACA TGC CCC CAG CAC TTG AAA Leu Tyr Gly Pro Lys Ile Asp Arg Ala Thr Cys Pro Gln His Leu Lys 400 405 410	1251
TGG AAA GAT AAA ACG AGA CAC GTC CTG CAG TGC CAA GCC AGG GGC AAC Trp Lys Asp Lys Thr Arg His Val Leu Gln Cys Gln Ala Arg Gly Asn 415 420 425	1299
CCG TAC CCC GAG CTG CGG TGT TTG AAG GAA GGC TCC AGC CGG GAG GTG Pro Tyr Pro Glu Leu Arg Cys Leu Lys Glu Gly Ser Ser Arg Glu Val 430 435 440	1347
CCG GTG GGG ATC CCG TTC GTC AAC GTA ACA CAT AAT GGT ACT TAT Pro Val Gly Ile Pro Phe Phe Val Asn Val Thr His Asn Gly Thr Tyr 445 450 455 460	1395
CAG TGC CAA GCG TCC AGC TCA CGA GGC AAA TAC ACC CTG GTC GTG GTG Gln Cys Gln Ala Ser Ser Ser Arg Gly Lys Tyr Thr Leu Val Val Val 465 470 475	1443
ATG GAC ATT GAG GCT GGG AGC TCC CAC TTT GTC CCC GTC TTC GTG GCG Met Asp Ile Glu Ala Gly Ser Ser His Phe Val Pro Val Phe Val Ala 480 485 490	1491
GTG TTA CTG ACC CTG GGC GTG GTG ACT ATC GTA CTG GCC TTA ATG TAC Val Leu Leu Thr Leu Gly Val Val Thr Ile Val Leu Ala Leu Met Tyr 495 500 505	1539

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGAACGCTC CTCGGCCTCT GGTCTNCTCT GNCGCTGGGG ATCCTAGGCA TCTCAGGTA 60
GAAGAGCCCCG CCCGTGGAGC NAGGTGGATA AGGCGGGGGC GGAATTGAAG GACCAGAGAG 120
GGCGGCCCGG GTGTCCCCCT CCAGGCTCCG CCCTCTTCTA GCTTCCCACG CTTCTGTAC 180
CACCTGGAGN TCGGGGCTTC TCCCCGTCTT TCCTCCACCC CAACACACCT CAATCTTCA 240
GANCTGAACC CAGCACCTT TCTGGANTNG GGGNNNTTGCA CCTAACCTGT CTCAGGAGAN 300
ACTGTGGCTC TCCTGTCCCTC TCCTGCTCTG TNATGCCCTA TGGTTCACAG ACTGGCATCA 360
TCCCTATTCA TGATCCTCAA AGACNCCATC TCCTCAACTG TCATAACTCA GAGCTCTATT 420
CCCCCTCCAC CTGGAGGCCCT GGAAACCGGC TTTCTAGGGC TTTTCTCCGC GGTTCTTCC 480
CGGAGTCAG CGTTGTGGCT TTTTGTCCAA GTTACTCAAG TTTGGGGACA ATCTCCTTTA 540
AGCCTTGAC TCAGTCTCAT TTCCACTTTG CTTTTGCCCT AAGCCTCTGT GTCTCTCCCC 600
CATTTCCCTGA CGATCTGTCA GAGTCTTAAG AGTGATTTGG TTCCCCATCC CCCCTCCAAC 660
TGGAGTCTCC TCCTCACTAT TGATGTGTGC ATCTGAGACC CCCATCCCCG CACCGAGITT 720
CCCCATCTCT GTCAGTAAAG AGCAAGGCTT CCAGAGACAA CCCTCTAATA GCGCGTCAGT 780
CCCGAATCTT GAGTGGGATG CGGGACTCCC GTGCTATTTC TTGGCGGAGG TCTTTCTGG 840
TCCTTATGGA CACCCCTGGT TTGGGATATG GGGGCCGCTA AGATTTCAGA GATGGGGTCC 900
CTAGGCTGAG NCCCGGTTTT CCCGGGCAGC GGTCGCGCTA GAACCTTCTT GGGCGGACCT 960
TCAGCCCCGC GTGGCGCTCG TGGAGCGCGG GGGCTCGCTG TGGCTCAACT GCAGCACTAA 1020
CTGTCCGAGG CCGGAGCGCG GGGCCCTGGA GACCTCGCTA CGCCGAAACG GGACCCAGAG 1080

GGGTCTGNAC TGNCTGGCTC GACAGCTGGT GGACATCCGA GANCCTGAAA CCCAGCCGGT	1140
CTGCTTCCTTC CNCTGCCGC GCCGCACACT CCAAGCGCGT GGGCTCATCC GAACTTCCG	1200
TGAGTTCAAG GTGGGCACNC CCCTTGGTC TCTGGACCTC CCCCTCAAGC TCCTCCCACC	1260
CGCCCTCTGA TCCTCCTGCT TGTTCTGAAA GTACTACAGC TGGCTAGAGC GGAGTTTTG	1320
GTCCTTGCA GAGCGACCGG ATCGGGTAGA GCTAGTGCCT CTGCCTCCCTT GGCAAGCCTGT	1380
AGGTGAGAAC TTCACCTTGA GCTGCAGGGT CCCGGGGCA GGACCCCGAG CGAGCCTCAC	1440
ATTGACCTTG CTGCGAGGCG GCCAGGAGCT GATTGCCGA AGTTCTGTAG GCGAGCCACC	1500
CCGAGCTCGG GGTGCGATGC TCACCGCCAC GGTCCTGGCG CGCAGAGAGG ATCACAGGC	1560
CAATTCTCA TGCCTCGCGG AGCTTGACCT GCGNCCACAC GGCTTGGGAC TGTTGCANA	1620
CAGCTCAGCC CCCAGACAGC TCCGCACGTT TGGTGAGTGT GGACCCCTAAC TGACAGATTT	1680
TAAGAAGTTT AGGGCAGCCA GGCGTGGTGG CATGGTGTG TAGGCCCTAA GTCCCAGCCC	1740
AAGCAGANCT AAGNCGGATC TCTTGTGAAT TAAAAGTCTA GCTCGTCTAC ATAACGAGGN	1800
CTGCATAGTT AAATCCCCCA AAAGTCTAAG CAGCTAGCCC TTACTTCAA CACAAGTACT	1860
AGCTTAAGTA CTTTCTCCTG TGAGCTTTT CCTTTATGTA TTTACTCGTT GAGAGAAAAA	1920
GAGAGTGTGT GTACGTGCCT TTATGCACAT GCCGCAGTGC TTGTATGGAA GTTAAAGAAT	1980
AAGGAGGCGT TCTGCCCTTC CATCCTGTGG GTCCTAGGGG TGGTATTAGC TCCTCAGGCT	2040
TTGTTAGTNA CAAGCGCTA GGCTTGGGGA GCCATCTCGC CCGCTCCTCT GTATCTTAG	2100
GGTGAAACCA GACAATGCAT GCAAATTGGT TGATCAACAC TGAATGTTA GTTCGTAAAT	2160
TCAAGCTCTG TTCTTTGTCT TCCTCAGCCA TGCCTCCACT TTCCCCCGAG CCTTATTGCC	2220
CCACGATTCT TAGAAGTGGG CTCAGAAAGG CCGGTGACKT GCACCTTGGA TGGACTGTT	2280
CCTGCCCTCAG AAGCCGGGT TTACTTCTCT CTGGGAGATC AGAGGCTTCA TCCTAATGTG	2340
ACCCTCGACG GGGAGAGCCT TGTGGCCACT GCCACAGCTA CAGCAAGTGA AGAACAGGAA	2400
GGCACCAAAAC AGCTGATGTG CATCGTGACC CTCGGGGCG AAAGCAGGGA GACCCAGGAA	2460
AACCTGACTG TCTACAGTAA GGGGAATCCA ACAAGACCTT CAATAGCTCA GACTGGGCT	2520
GGGGCTGGGT CTGGGTCTGG GGCCAGAGTC TCACAAAGGC GGAGCCTATA AAGTGGCGG	2580
GACCTCCACA CCAGAACAAAG CCGGGCGGGGA GAGTTCCAGG GCAGGAGCAG ATAGAAGTTG	2640
GAAATTAATA GATTGGGTTG AGTCCCTGA GTGGGGAGTG AACCCCACCC AATTCTCTGT	2700
CCCCAGGCTT CCCGGCTCCT CTTCTGACTT TAAGTGAGCC AGAAGCCCC GAGGGAAAGA	2760
TGGTGACCGT AAGCTGCTGG GCAGGGGCC CAGCCCTTGT CACCTTGGAG GGAATTCCAA	2820
GGACCCCTTT ACCGGCCCCA TCTTTAACCT TATCGTATCC CCTCTGCCCTC ATGCCCGCAG	2880
ACGCACCTCG GCTGGATGAC TTGGACTGTC CCAGGAGCTG GACGTGGCCA GAGGGTCCAG	2940
AGCAGACCCT CCACTGCGAG GCCCGTGGAA ACCCTGAGCC CTCCGTGCAC TGTGCAAGGC	3000

CTGACGGTGG GGCGGTGCTA GCGCTGGGCC TGTTGGGTCC AGTGACCCGT GCCCTCGCGG	3060
GCACTTACCG ATGTACAGCA ATCAATGGGC AAGGCCAGGC GGTCAAGGAT GTGACCCCTGA	3120
CTGTGGAATG TGAGTAGGGG GAGGTGGCA TGCTTATCCC TTTAAGGTCA CGGAGTGTAC	3180
TGGGAGACTG GCTATACGGA AAGGAAAGAA GCCTAGGTTC AGCAGGGATT GGGAAAACAC	3240
TGAAGGAAAG TGGTGTGGTG TTTACAAACT TAACGGTGGT AACTGGGCAC GGTCTGGCAA	3300
AAACAGACAG CCAAGAGAGT GTGCCCTGGGA AGCTGCAATG GGGGCTTGT GGGAAATTGGT	3360
CAACAGCACC CTGAGATCTC AGGAAAGGGG CCTGAAGTTA TCTCCAGAAC CCATGTGAAG	3420
GCAGGAAGAG AGAACGCCA CCTTTTCCTG CTCCCCCAA CCCCCCCCCA CATATCACAC	3480
GGAGTATATA AATAAATAAA ATGGCTCCTG CCGGAGGGAG TGAGAAGCTG TCTCCTGCAG	3540
GCTCAGAGCA GTGGTAGTGC ATGCCTTAA TCCCAGCACT CGGTAGGCAA AGGCAGGCAG	3600
ATCTCTGTGA ATGTGGGCC AGCCTGGTCT GTACAGAGAA ATCCTGTCTC AAAACAAACC	3660
AGCAAAGAAA CAAAACAAA ATCAATTCCA GATGCCCAAG CGCTGGACAG TGTAGGCTGC	3720
CCANGACGTA TTACTTGNCT GGAGGGGACA GAGGCATCGC TTAGCTGTGT GGCACACGGG	3780
GTCCCACCAC CTAGCGTGAG CTGTGTGCGC TCTGGAAAGG AGGAAGTCAT GGAAGGGCCC	3840
CTGCGTGTGG CCCGGGAGCA CGCTGGCACT TACCGATGCG AAGCCATCAA CGCCAGGGGA	3900
TCAGCGGNCA AAAATGTGGC TGTCACGGTG GAATGTGAGT AGGGGTGGCT ACGGAAATGT	3960
CCACACCTGC GTCCTCTGTC CTCAGTGTGA ACTCCTATTT CCCTGCTTCC TAGATGGTCC	4020
CAGTTNTGAG GAGTTGGGCT GCCCCAGCAA CTGGACTTGG GTAGAAGGAT CTGGAAAACT	4080
GTTTCCTGT GAAGTTGATG GGAAGCCGGA ACCACCGTG GAGTGCCTGG GCTCGGAGGG	4140
TGCAAGCGAA GGGTAGTGT TGCCCCCTGGT GTCCTCGAAC TCTGGTTCCA GAAACTCTAT	4200
GACTCCTGGT AACCTGTAC CGGGTATTTA CCTCTGCAAC GCCACCAACC GGCACTGGCTC	4260
CACAGTCAAA ACAGTCGTCG TGAGCGCGGA ATGTGAGCAG GGGCCCAGGT GGGCGGAGAG	4320
TACCGGGTGT CCCAGGATCT TTTCTTCCC TGATGCCCT CCTTATGGTG GCTGATCTGC	4380
AGCACCGCCA CAGATGGATG AATCCAGTTG CCCGAGTCAC CAGACATGGC TGGAAGGAGC	4440
CGAGGCTACT GCGCTGGCCT GCAGTGACAG GGGNCGGCCC TCTCCACGCG TGCGCTGTTC	4500
CAGGGAAGGT GCAGCCAGGC TGGAGAGGCT ACAGGTGTCC CGAGAGGATG CGGGGACCTA	4560
CCTGTGTGTG GCTACCAACG CGCATGGCAC GGATTACCGG ACCGTCACTG TGGGTGTGGA	4620
ATGTGAGTGA GGACAGCGCT GAATGAAGAC GACTCAGACC GCCAGAAAAG TGCCTTGAGG	4680
CCTGGGATGT ATGATCCAGT GGGTAGAGTG CTCAATTAGC ACTCACTAAA ATGTATATTC	4740
TATTCTTAAT ACTCTTTAAT TTTANCCCTT GGGAGGCAGA GACAGGCAGA TCTCTGTTCC	4800
GGGATAACCT GCTCTCTGTC TAGGACAGCT TGGTCTACAG AGGGGNTACA GGCCCCCCT	4860
CCCAAGATTG NATAGCAACC CTCTGGCTCC CTGTCTCTCT	4900

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

NGAATTCCGG CGGATCGGGT AGAGCTAGTG CCTCTGCCTC CTTGGCAGCC TGTAGGTGAG	60
AACTTCACCT TGAGCTGCAG GGTCCCGGGG GCAGGACCCC GAGCGAGCCT CACATTGACC	120
TTGCTGCGAG GCGGCCAGGA GCTGATTGCG CGAAGTTCG TAGGCGAGCC ACCCCGAGCT	180
CGGGGTGCAG TGCTCACCGC CACGGTCCTG GCGCGCAGAG AGGATCACAG GGCAATTTC	240
TCATGCCTCG CGGAGCTTGA CCTGCGGCCA CACGGCTTGG GACTGTTGC AAACAGCTCA	300
GCCCCCAGAC AGCTCCGCAC GTTGCCATG CCTCCACTTT CCCCAGCCT TATTGCCCA	360
CGATTCTTAG AAGTGGGCTC AGAAAGGCCG GTGACTTGCA CTTTGGATGG ACTGTTCC	420
GCCCCAGAAG CCGGGGTTTA CCTCTCTCTG GGAGATCAGA GGCTTCATCC TAATGTGACC	480
CTCGACGGGG AGAGCCTTGT GGCCACTGCC ACAGCTACAG CAAGTGAAGA ACAGGAAGGC	540
ACCAAACAGC TGATGTGCAT CGTGACCCCTC GGGGGCGAAA GCAGGGAGAC CCAGGAAAAC	600
CTGACTGTCT ACAGCTTCCC GGCTCCTCTT CTGACTTTAA GTGAGCCAGA AGCCCCCGAG	660
GGAAAGATGG TGACCGTAAG CTGCTGGCA GGGGCCGAG CCCTTGTAC CTTGGAGGGA	720
ATTCCAAGGA CCCTCTTACC GGCCCCATCT TTAACCTTAT CGTATCCCCT CTGCCTCATG	780
CCCGCAGACG CACCTCGGCT GGATGACTTG GACTGTCCC GGAGCTGGAC GTGCCAGAG	840
GGTCCAGAGC AGACCCTCCA CTGCGAGGCC CGTGGAAACC CTGAGCCCTC CGTGCAGTGT	900
GCAAGGCCTG ACGGTGGGGC GGTGCTAGCG CTGGGCCTGT TGGGTCCAGT GACCCGTGCC	960
CTCGCGGGCA CTTACCGATG TACAGCAATC AATGGGAAG GCCAGGCGGT CAAGGATGTG	1020
ACCCCTGACTG TGGAATATGC CCCAGCGCTG GACAGTGTAG GCTGCCAGA ACGTATTACT	1080
TGGCTGGAGG GGACAGAGGC ATCGCTTAGC TGTGTGGCAC ACGGGGTCCC ACCACCTAGC	1140
GTGAGCTGTG TGCGCTCTGG AAAGGAGGAA GTCATGGAAG GGCCCTGCG TTTTGGCCGG	1200
GAGCACGCTG GCACTTACCG ATGCGAAGCC ATCAACGCCA GGGGATCAGC GGCCAAAAAT	1260
GTGGCTGTCA CGGTGGAATA TGGTCCCCGG AATTC	1295

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGAACATTTGA	GTGGGATGCG	GGACTCCCGT	GCTATTCTT	GGCGGAGGTC	TTTCCTGGTC	60
CTTATGGACA	CCCCTGGTTT	GGGATATGGG	GGCCGCTAAG	ATTCAGAGA	TGGGGTCCCT	120
AGGCTGAGCC	CGCGTTTCC	CGGGCAGCGG	TCGCCTAGA	ACCTTCTGG	GCGGACCTTC	180
AGCCCCGCGT	GGCGCTCGTG	GAGCGCGGGG	GCTCGCTGTG	GCTCAACTGC	AGCACTAACT	240
GTCCGAGGCC	GGAGCGCGGT	GGYCTGGAGA	CCTCGCTACG	CCGAAACGGG	ACCCAGAGGG	300
GTCTGCGCTG	GCTGGCTCGA	CAGMTGGTGG	ACATCCGAGA	GCCTGAAACC	CAGTCGGTCT	360
GCTTCTTCCG	CTGGGCGCGC	CGCACACTCC	AAGNGAGTGG	GCTCATCCGA	ACTTTCCAGC	420
GACCGGATCG	GGTAGAGCTA	GTGCCTCTGN	CTCCTGGCA	GCCTGTAGGT	GAGAACTTCA	480
CCTTGAGCTG	CAGGGTCCCG	GGGGCAGGAC	CCCGAGCGAG	CCTCACATTG	ACCTTGCTGC	540
GAGGCGGCCA	GGAGCTGATT	CGCCGAAGTT	TCGTAGGCAG	GCCACCCCGA	GCTCGGGGTG	600
CGATGCTCAC	CGCCACGGTC	CTGGCGCGCA	GAGAGGATCA	CAGGGCCAAT	TTCTCATGCC	660
TCGCGGAGCT	TGACCTGCGG	ACACACGGCT	TGGGACTGTT	TGCAAACAGC	TCAGCCCCA	720
GACAGCTCCG	CACGTTGGC	ATGCCTCCAC	TTTCCCCGAG	CCTTATTGNC	CCACGATTCT	780
TAGAAGTGGG	CTCAGAAAGG	CCGGTGACTT	GCACTTGGA	TGGACTGTTT	CCTGCCAG	840
AAGCCGGGT	TTACCTCTCT	CTGGGAGATC	AGAGGCTTCA	TCCTTAATGTG	ACCCTCGACG	900
GGGAGAGCCT	TGTGGCCACT	GNCACAGMTA	CAGCAAGTGA	AGAACAGGAA	GGCACCAAAC	960
AGCTGATGTG	CATCGTGACC	CTCGGGGGCG	AAAGCAGGGA	GACCCAGGAA	AACCTGACTG	1020
TCTACAGCTT	CCCGGCTCCT	CTTCTGACTT	TAAGTGAGCC	AGAAGCCCC	GAGGGAAAGA	1080
TGGTGACCGT	AAGCTGCTGG	GCAGGGGCC	GAGCCCTTGT	CACCTTGGAG	GGAATTCCAG	1140
CTGCGGTCCC	TGGGCAGCCC	GCTGAGCTCC	AGTTAAATGT	CACAAAGAAT	GACGACAAGC	1200
GGGGCTCTT	CTGCGACGCT	GCCCTCGATG	TGGACGGGGA	AACTCTGAGA	AAGAACCCAGA	1260
GCTCTGAGCT	TCGTGTTCTG	TACGCACCTC	GGCTGGATGA	CTTGGACTGT	CCCAGGAGCT	1320
GGACGTGGCC	AGAGGGTCCA	GAGCAGACCC	TCCACTGCGA	GGCCCGTGGA	AACCTGAGC	1380
CCTCCGTGCA	CTGTGCAAGG	CCTGACGGTG	GGCGGTGCT	AGCGCTGGC	CTGTTGGTC	1440
CAGTGACCCG	TGCCCTCCCG	GGAACTTACC	GATGTACAGC	AATCAATGGG	CAAGGCCAGG	1500
CGGTCAAGGA	TGTGACCTG	ACTGTGGAAT	ATGCCCAAGC	GCTGGACAGT	GTAGGCTGCC	1560
CAGAACGTAT	TACTTGGCTG	GAGGGGACAG	AGGCATCGCT	TAGCTGTGTG	GCACACGGGG	1620
TCCCCACCACC	TAGCGTGAGC	TGTGTGCGCT	CTGGAAAGGA	GGAAGTCATG	GAAGGGCCCC	1680
TGCGTGTGGC	CCGGGAGCAC	GCTGGCACTT	ACCGATGCGA	AGCCATCAAC	GNCAGGGGAT	1740
CAGCGGWCAA	AAATGTGGCT	GTCACGGTGG	AAATGGTCC	CAGTTGGAG	GAGTTGGGCT	1800

GCCCCAGYAA	CTGGACTTGG	GTAGAAGGAT	CTGGAAAAC	GTTTCCTGT	GAAGTTGATG	1860
GGAAGCCGGA	ACCACGCGTG	GAGTGCCTGG	GCTCGGAGGG	TGCAAGCGAA	GGGGTAGTGT	1920
TGCCCTGGT	GTCCTCGAAC	TCTGGTTCCA	GAAACTCTAT	GACTCCTGGT	AACCTGTCAC	1980
CGGGTATTAA	CCTCTGCAAC	GCCACCAACC	GGMATGGNTC	CACAGTCAAA	ACAGTCGTCG	2040
TGAGCGCGGA	ATCACCGCCA	CAGATGGATG	AATCCAGTTG	CCCGAGTCAC	CAGACATGGN	2100
TGGAAGGAGC	CGAGGNTACT	GCGCTGGCCT	GCAGTGCCAG	AGGNCGCCCC	TCTCCACGCG	2160
TGCGCTGTT	CAGGGAAAGGT	GCAGMCAGGC	TGGAGAGGNT	ACAGGTGTCC	CGAG	2214

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5077 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGAACGCTC	CTCGGCCTCT	GGTCTNCTCT	GGNCCTGGGG	ATCCTAGGCA	TCTCAGGTAA	60
GAAGAGCCCG	CCC GTGGAGC	NAGGTGGATA	AGGCGGGGGC	GGAAATTGAAG	GACCAGAGAG	120
GGCGGCCCGG	GTGTCCCCCT	CCAGGCTCCG	CCCTCTTCTA	GCTTCCCACG	CTTCTGTCAC	180
CACCTGGAGN	TCGGGGCTTC	TCCCCGTCTT	TCCTCCACCC	CAACACACCT	CAATCTTCA	240
GANCTGAACC	CAGCACCTTT	TCTGGANTNG	GGGNNTTGCA	CCTAACCTGT	CTCAGGAGAN	300
ACTGTGGCTC	TCCTGTCTCT	TCCTGCTCTG	TNATGCCCTA	TGGTTCACAG	ACTGGCATCA	360
TCCCTATTCA	TGATCCTCAA	AGACNCCATC	TCCTCAACTG	TCATAACTCA	GAGCTCTATT	420
CCCCCTCCAC	CTGGAGCCCT	GGAAACCGGC	TTTCTAGGGC	TTTTCTCCGC	GGTTCTTTCC	480
CGGAGTTCA	CGTTGTGGCT	TTTTGTCAA	GTTACTCAAG	TTTGGGGACA	ATCTCCTTTA	540
AGCCTTGAC	TCAGTCTCAT	TTCCACTTTG	CTTTTGCCCC	AAGCCTCTGT	GTCTCTCCCC	600
CATTTCCTGA	CGATCTGTCA	GAGTCTTAAG	AGTGATTGG	TTCCCCATCC	CCCCTCCAAC	660
TGGAGTCTCC	TCCTCACTAT	TGATGTGTGC	ATCTGAGACC	CCCATCCCCG	CACCGAGTTT	720
CCCCATCTCT	GTCAGTAAAG	AGCAAGGCTT	CCAGAGACAA	CCCTCTAATA	GCGCGTCAGT	780
CCCGAATCTT	GAGTGGGATG	CGGGACTCCC	GTGCTATTT	TTGGCGGAGG	TCTTCCTGG	840
TCCTTATGGA	CACCCCTGGT	TTGGGATATG	GGGGCCGCTA	AGATTTCAGA	GATGGGGTCC	900
CTAGGCTGAG	NCCCGTTTT	CCCGGGCAGC	GGTCGCGCTA	GAACCTTTCT	GGCGGGACCT	960
TCAGCCCCGC	GTGGCGCTCG	TGGAGCGCGG	GGGCTCGCTG	TGGCTCAACT	GCAGCACTAA	1020
CTGTCCGAGG	CCGGAGCGCG	GTGGCCTGGA	GACCTCGCTA	CGCCGAAACG	GGACCCAGAG	1080
GGGTCTGNAC	TGNCTGGCTC	GACAGCTGGT	GGACATCCGA	GANCCTGAAA	CCCAGCCGGT	1140

CTGCTTCTTC CNCTGCCGC GCCGCACACT CCAAGCGCGT GGGCTCATCC GAACTTCCG	1200
TGAGTTCAAGG GTGGGCACNC CCCTTGGTC TCTGGACCTC CCCCTCAAGC TCCTCCCACC	1260
CGCCCTCTGA TCCTCTGCT TGTCTGAAA GTACTACAGC TGGCTAGAGC GGAGTTTTG	1320
GTCCCTTGCA GAGCGACCGG ATCGGGTAGA GCTAGTGCCT CTGCCTCCTT GGCAGCCTGT	1380
AGGTGAGAAC TTCACCTTGA GCTGCAGGGT CCCGGGGCA GGACCCCGAG CGAGCCTCAC	1440
ATTGACCTTG CTGCGAGGCG GCCAGGAGCT GATTGCCGA AGTTTCGTAG GCGAGCCACC	1500
CCGAGCTCGG GGTGCGATGC TCACCGCCAC GGTCTGGCG CGCAGAGAGG ATCACAGGGC	1560
CAATTCTCA TGCCTCGCG AGCTTGACCT GCGNCCACAC GGCTTGGGAC TGTTGCANA	1620
CAGCTCAGCC CCCAGACAGC TCCGCACGTT TGGTGAGTGT GGACCCCTAAC TGACAGATTT	1680
TAAGAAGTTT AGGGCAGCCA GGCCTGGTGG CATGGTGTG TAGGCCCTAA GTCCCAGCCC	1740
AAGCAGANCT AAGNCGGATC TCTTGTGAAT TAAAAGTCTA GCTCGTCTAC ATAACGAGGN	1800
CTGCATAGTT AAATCCCCCA AAAGTCTAAG CAGCTAGCCC TTACTTCCAA CACAAGTACT	1860
AGCTTAAGTA CTTTCTCCTG TGAGCTTTT CCTTTATGTA TTTACTCGTT GAGAGAAAAA	1920
GAGAGTGTGT GTACGTGCCT TTATGCACAT GCCGCAGTGC TTGTATGGAA GTTAAAGAAT	1980
AAGGAGGCCT TCTGCCCTTC CATCCTGTGG GTCCTAGGGG TGGTATTAGC TCCTCAGGCT	2040
TTGTTAGTNA CAAGCGCTA GGCTTGGGA GCCATCTCGC CCGCTCCTCT GTATCTTAG	2100
GGTAAACCA GACAATGCAT GCAAATTGGT TGATCAACAC TGAATGTTA GTTCGTAAAT	2160
TCAAGCTCTG TTCTTGTCT TCCTCAGCCA TGCCTCCACT TTCCCCGAG CCTTATTGCC	2220
CCACGATTCT TAGAAGTGGG CTCAGAAAGG CCGGTGACKT GCACTTGGA TGGACTGTT	2280
CCTGCCCTAG AAGCCGGGT TTACTTCTCT CTGGGAGATC AGAGGCTTCA TCCTAATGTG	2340
ACCTCGACG GGGAGAGCCT TGTGCCACT GCCACAGCTA CAGCAAGTGA AGAACAGGAA	2400
GGCACCAAAAC AGCTGATGTG CATCGTGACC CTCGGGGCG AAAGCAGGGA GACCCAGGAA	2460
AACCTGACTG TCTACAGTAA GGGGAATCCA ACAAGACCTT CAATAGCTCA GACTGGGCT	2520
GGGGCTGGGT CTGGGTCTGG GGCCAGAGTC TCACAAAGGC GGAGCCTATA AAGTGGCGG	2580
GACCTCCACA CCAGAACAAAG CCGGGCGGGGA GAGTCCAGG GCAGGAGCAG ATAGAAGTTG	2640
GAAATTATA GATTGGGTTG AGTCCCTGA GTGGGGAGTG AACCCACCC AATTCTCTGT	2700
CCCCAGGCTT CCCGGCTCCT CTTCTGACTT TAAGTGAGCC AGAAGCCCC GAGGGAAAGA	2760
TGGTGACCGT AAGCTGCTGG GCAGGGGCC GAGCCCTGT CACCTTGGAG GGAATTCCAG	2820
CTGCGGTCCC TGGGCAGCCC GCTGAGCTCC AGTTAAATGT CACAAAGAAT GACGACAAGC	2880
GGGGCTTCTT CTGCGACGCT GCCCTCGATG TGGACGGGGAA AACTCTGAGA AAGAACAGA	2940
GCTCTGAGCT TCGTGTCTG TGTGAGTGGAA TGTTCACTTT ATCTCTGTGA ATTCCAAGGA	3000
CCCTCTTACC GGCCCCATCT TTAACCTTAT CGTATCCCCT CTGCCTCATG CCCGCAGACG	3060

CACCTCGGCT GGATGACTTG GACTGTCCCA GGAGCTGGAC GTGCCAGAG GGTCCAGAGC	3120
AGACCCCTCCA CTGCGAGGCC CGTGGAAACC CTGAGCCCTC CGTGCAGTGT GCAAGGCCTG	3180
ACGGTGGGCG GGTGCTAGCG CTGGGCCTGT TGGGTCCAGT GACCCGTGCC CTCGCAGGCA	3240
CTTACCGATG TACAGCAATC AATGGGCAAG GCCAGGCGGT CAAGGATGTG ACCCTGACTG	3300
TGGAATGTGA GTAGGGGAG GTGGGCATGC TTATCCCTTT AAGGTCACGG AGTGTACTGG	3360
GAGACTGGCT ATACGGAAAG GAAAGAAGGCC TAGGTTCAGC AGGGATTGGG AAAACACTGA	3420
AGGAAAGTGG TGTGGTGTGTT ACAAACTTAA CGGTGGTAAC TGGGCACGGT CTGGCAAAAA	3480
CAGACAGCCA AGAGAGTGTG CCTGGGAAGC TGCAATGGGG GCTTGTGGG AATTGGTCAA	3540
CAGCACCCCTG AGATCTCAGG AAAGGGCCT GAAGTTATCT CCAGAACCCA TGTGAAGGCA	3600
GGAAGAGAGA ACGCCCACCT TTTCCTGCTC CCCCCAACCC CCCCCCACAT ATCACACGGA	3660
GTATATAAAAT AAATAAAATG GCTCCTGCCG GAGGGAGTGA GAAGCTGTCT CCTGCAGGCT	3720
CAGAGCAGTG GTAGTGCATG CCTTTAATCC CAGCACTCGG TAGGCAAAGG CAGGCAGATC	3780
TCTGTGAATG TGGGGCCAGC CTGGTCTGTA CAGAGAAATC CTGTCTCAAA ACAAAACCAGC	3840
AAAGAAACAA AACCAAAATC AATTCCAGAT GCCCCAGCGC TGGACAGTGT AGGCTGCCA	3900
NGACGTATTA CTTGNCTGGA GGGGACAGAG GCATCGCTTA GCTGTGTGGC ACACGGGTC	3960
CCACCAACCTA GCGTGAGCTG TGTGCGCTCT GGAAAGGAGG AAGTCATGGA AGGGCCCTG	4020
CGTGTGGCCC GGGAGCACGC TGGCACTTAC CGATGCGAAG CCATCAACGC CAGGGATCA	4080
GCGGNCAAAA ATGTGGCTGT CACGGTGGAA TGTGAGTAGG GGTGGCTACG GAAATGTCCA	4140
CACCTGCGTC CTCTGTCCTC AGTGTGAAC CCTATTCCTC TGCTTCCTAG ATGGTCCCAG	4200
TTNTGAGGAG TTGGGCTGCC CCAGCAACTG GACTTGGTA GAAGGATCTG GAAAACGTGTT	4260
TTCCTGTGAA GTTGATGGGA AGCCGGAACC ACGCGTGGAG TCGGTGGCT CGGAGGGTGC	4320
AAGCGAAGGG GTAGTGTTCGC CCCTGGTGTC CTCGAACCTCT GGTTCCAGAA ACTCTATGAC	4380
TCCTGGTAAC CTGTCACCGG GTATTTACCT CTGCAACGCC ACCAACCGGC ATGGCTCCAC	4440
AGTCAAAACA GTCGTCGTGA GCGCGGAATG TGAGCAGGGG CCCAGGTGGG CGGAGAGTAC	4500
CGGGTGTCCC AGGATCTTT CTTTCCCTGA TGCCCCTCCT TATGGTGGCT GATCTGCAGC	4560
ACCGCCACAG ATGGATGAAT CCAGTTGCC GAGTCACCAAG ACATGGCTGG AAGGAGCCGA	4620
GGCTACTGCG CTGGCCTGCA GTGACAGGGG NCGCCCTCT CCACCGGTGC GCTGTTCCAG	4680
GGAAGGTGCA GCCAGGCTGG AGAGGCTACA GGTGTCCCGA GAGGATGCGG GGACCTACCT	4740
GTGTGTGGCT ACCAACGCAGC ATGGCACCGA TTCACGGACC GTCACTGTGG GTGTGGAATG	4800
TGAGTGAGGA CAGCGCTGAA TGAAGACGAC TCAGACCGCC AGAAAAGTGC CTTGAGGCCT	4860
GGGATGTATG ATCCAGTGGG TAGAGTGCCTC AATTAGCACT CACTAAAATG TATATTCTAT	4920
TCCTTAATACT CTTTAATTTC ANCCTTTGGG AGGCAGAGAC AGGCAGATCT CTGTTCCGGG	4980

ATAACCTGCT CTCTGTCTAG GACAGCTTGG TCTACAGAGG GGNTACAGGC CCCCCCTCCC	5040
AAGATTGNAT AGCAACCCTC TGGCTCCCTG TCTCTCT	5077

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

NGAATTCCGG CGGATCGGGT AGAGCTAGTG CCTCTGCCTC CTTGGCAGCC TGTAGGTGAG	60
AACTTCACCT TGAGCTGCAG GGTCCCGGGG GCAGGACCCC GAGCGAGCCT CACATTGACC	120
TTGCTGCGAG GCGGCCAGGA GCTGATTGCG CGAAGTTCG TAGGCGAGCC ACCCCGAGCT	180
CGGGGTGCGA TGCTCACCGC CACGGTCCTG GCGCGCAGAG AGGATCACAG GGCAATTTC	240
TCATGCCTCG CGGAGCTTGA CCTGCGGCCA CACGGCTTGG GACTGTTTGC AAACAGCTCA	300
GCCCCCAGAC AGCTCCGCAC GTTGCCATG CCTCCACTTT CCCCAGGCCT TAATGCCCCA	360
CGATTCTTAG AAGTGGGCTC AGAAAGGCCG GTGACTTGCA CTTTGGATGG ACTGTTTCCT	420
GCCCCAGAAG CCGGGGTTTA CCTCTCTCTG GGAGATCAGA GGCTTCATCC TAATGTGACC	480
CTCGACGGGG AGAGCCTTGT GGCCACTGCC ACAGCTACAG CAAGTGAAGA ACAGGAAGGC	540
ACCAAAACAGC TGATGTGCAT CGTGACCCCTC GGGGGCGAAA GCAGGGAGAC CCAGGAAAAC	600
CTGACTGTCT ACAGCTTCCC GGCTCCTCTT CTGACTTTAA GTGAGCCAGA AGCCCCCGAG	660
GGAAAGATGG TGACCGTAAG CTGCTGGCA GGGGCCGAG CCCTTGTCAC CTTGGAGGGA	720
ATTCCAGCTG CGGTCCCTGG GCAGCCCGCT GAGCTCCAGT TAAATGTCAC AAAGAATGAC	780
GACAAGCGGG GCTTCTCTG CGACGCTGCC CTCGATGTGG ACGGGGAAAC TCTGAGAAAG	840
AACCAGAGCT CTGAGCTTCG TGTCTGTGT GAGTGGATGT TCACCTTATC TCTGTGAATT	900
CCAAGGACCC TCTTACCGGC CCCATTTTA ACCTTATCGT ATCCCTCTG CCTCATGCC	960
GCAGACGCAC CTCGGCTGGA TGACTTGGAC TGTCCCAGGA GCTGGACGTG GCCAGAGGGT	1020
CCAGAGCAGA CCCTCCACTG CGAGGCCCGT GGAAACCTG AGCCCTCCGT GCACTGTGCA	1080
AGGCCTGACG GTGGGGCGGT GCTAGCGCTG GGCCTGTTGG GTCCAGTGAC CCGTGCCCTC	1140
GCGGGCACCT ACCGATGTAC AGCAATCAAT GGGCAAGGCC AGGCGGTCAA GGATGTGACC	1200
CTGACTGTGG AATATGCCCC AGCGCTGGAC AGTGTAGGCT GCCCAGAACG TATTACTTGG	1260
CTGGAGGGGA CAGAGGCATC GCTTAGCTGT GTGGCACACG GGGTCCCACC ACCTAGCGTG	1320
AGCTGTGTGC GCTCTGGAAA GGAGGAAGTC ATGGAAGGGC CCGTGCCTT TGGCCGGGAG	1380
CACGCTGGCA CTTACCGATG CGAAGCCATC AACGCCAGGG GATCAGCGGC CAAAAATGTG	1440

GCTGTCACGG TGGAATATGG TCCCCGGAAT TC

1472

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCTCTGCCTC CTTGGCAGCC TGTAGGTGAG AACTTCACCT TGAGCTGCAG GGTCCCGGGG	60
GCAGGACCCC GAGCGAGCCT CACATTGACC TTGCTGCGAG GCGGCCAGGA GCTGATT CGC	120
CGAAAGTTCG TAGGCGAGCC ACCCCGAGCT CGGGGTGCGA TGCTCACCGC CACGGTCCTG	180
GCGCGCAGAG AGGATCACAG GGCCAATTC TCATGCCTCG CGGAGCTTGA CCTGCGGCCA	240
CACGGCTTGG GACTGTTGC AACAGCTCA GCCCCCAGAC AGCTCCGCAC GTTGGCCATG	300
CCTCCACTTT CCCCAGCCT TATTGCCCA CGATTCTTAG AAGTGGGCTC AGAAAGGCCG	360
GTGACTTGCA CTTTGGATGG ACTGTTCCCT GCCCCAGAAC CGGGGGTTTA CCTCTCTCTG	420
GGAGATCAGA GGCTTCATCC TAATGTGACC CTCGACGGGG AGAGCCTTGT GGCCACTGCC	480
ACAGCTACAG CAACTGAAGA ACAGGAAGGC ACCAAACAGC TGATGTGCAT CGTGACCCCTC	540
GGGGCGAAA GCAGGGAGAC CCAGGAAAC CTGACTGTCT ACAGCTTCCC GGCTCCTCTT	600
CTGACTTTAA GTGAGCCAGA AGCCCCGAG GGAAAGATGG TGACCGTAAG CTGCTGGCA	660
GGGGCCCGAG CCCTTGTAC CTTGGAGGGG ATTCCAGCTG CGGTCCCTGG GCAGCCCGCT	720
GAGCTCCAGT TAAATGTCAC AAAGAATGAC GACAAGCGGG GCTTCTCTG CGACGCTGCC	780
CTCGATGTGG ACAGGGAAAC TCTGAGAAAG AACAGAGCT CTGAGCTTCG TGTTCTGTAC	840
GCACCTCGGC TGGATGACTT GGACTGTCCC AGGAGCTGGA CGTGGCCAGA GGGTCCAGAG	900
CAGACCCCTCC ACTGCGAGGC CCGTGGAAAC CCTGAGCCCT CCGTGCACTG TGCAAGGCCT	960
GACGGTGGGG CGGTGCTAGC GCTGGGCCTG TTGGGTCCAG TGACCCGTGC CCTCGCGGGC	1020
ACTTACCGAT GTACAGCAAT CAATGGCAA GGCCAGGCAG TCAAGGATGT GACCCTGACT	1080
GTGGAATATG CCCCAGCGCT GGACAGTGTA GGCTGCCAG AACGTATTAC TTGGCTGGAG	1140
GGGACAGAGG CATCGCTTAG CTGTGTGGCA CACGGGTCC CACCACCTAG CGTGAGCTGT	1200
GTGCGCTCTG GAAAGGAGGA AGTCATGGAA GGGCCCTGC GTGTGGCCCG GGAGCACGCT	1260
GGCACTTACC GATGCGAAGC CATCAACGCC AGGGGATCAG CGGCCAAAAA TGTGGCTGTC	1320
ACGGTGGAAAT ATGGTCCAG TTTTGAGGAG TTGGGCTGCC CCAGCAACTG GACTTGGGTA	1380
GAAGGATCTG GAAAATGTT TTCTGTGAA GTTGATGGGA AGCCGGAACC ACGCGTGGAG	1440
TGCGTGGGCT CGGAGGGTGC AAGCGAAGGG GTAGTGTGTC CCCTGGTGTGTC CTCGAACCTCT	1500

GGTTCCAGAA ACTCTATGAC TCCTGGTAAC CTGTCACCGG GTATTTACCT CTGCAACGCC	1560
ACCAACCGGC ATGGCTCCAC AGTCAAACA GTCGTCGTGA GCGCGGAATC ACCGCCACAG	1620
ATGGATGAAT CCAGTTGCC CAGTCACCAG ACATGGCTGG AAGGAGCCGA GGCTACTGCG	1680
CTGGCCTGCA GTGCCAGAGG CCGCCCCCTCT CCACGCGTGC GCTGTTCCAG GGAAGGTGCA	1740
GCCAGGCTGG AGAGGCTACA GGTGTCCCGA GAGGATGCGG GGACCTACCT GTGTGTGGCT	1800
ACCAACGCGC ATGGCACCGA TTCACGGACC GTCACTGTGG GTGTGGAATA CGGGCCTGTG	1860
GTGGCTGAGC TGGCAGCCTC GCCCCCCAAGC GTGCGGCCTG GCGGAAACTT CACTCTGACC	1920
TGCCGTGCAG AGGCCTGGCC TCCAGCCAG ATCAGCTGGC GCGCGCCCCC GGGAGCTCTC	1980
AACCTCGGTC TCTCCAGCAA CAACAGCAGC CTGAGCGTGG CGGGTGCCAT GGGCAGCCAT	2040
GGTGGCGAGT ATGAGTGCAG AGCCACCAAT GCGCATGGC GCCACGCACG GCGCATCACG	2100
GTGCGCGTGG CCGGTCCATG GCTGTGGGTC GCTGTGGGCG GTGCGGCAGG GGGCGCGCG	2160
CTGCTGGCCG CAGGGGCCGG CCTGGCCTTC TACGTGCAGT CCACCGCTTG CAAGAAGGGA	2220
GAGTACAACG TCCAGGAGGC TGAGAGCTCA GGCGAGGCAGG TGTGTCTCAA TGGCGCGGGC	2280
GGGACACCGG GTGCAGAAGG CGGAGCAGAG ACCCCCCGGCA CTGCCAGTC ACCTGCAGAT	2340
GGCGAGGTTT TCGCCATCCA GCTGACATCT TCCTGAGCCT GTATCCAGCT CCCCCAGGGG	2400
CCTCGAAAGC ACAGGGGTGG ACGTATGTAT TGTTCACTCT CTATTTATTAC AACTCCAGGG	2460
GCGTCGTCCC CGTTTCTAC CCATTCCCTT AATAAAGTTT TTATAGGAGA AAAAAAAA	2520
AAAAAAAAAA AAAAAAAA AAAAAAAA	2550

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AATTCGATCA CTCGCGCTCC CCTCGCCTTC TGCGCTCTCC CCTCCCTGGC AGCGGGCGCA	60
ATGCCGGGGC CTTCACCAGG GCTGCGCCGA ACGCTCCTCG GCCTCTGGGC TGCCCTGGGC	120
CTGGGGATCC TAGGCATCTC AGCGGTGCGC CTAGAACCTT TCTGGGCGGA CCTTCAGCCC	180
CGCGTGGCGC TCGTGGAGCG CGGGGGCTCG CTGTGGCTCA AC	222

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGTGGAGCTG GCACCCCTGC CTCCTTGGCA GCCGGTGGGC CAGAACTTCA CCCTGCGCTG	60
CCAAGTGGAG GGTGGGTCGC CCCGGACCAG CCTCACGGTG GTGCTGCTTC GCTGGGAGGA	120
GGAGCTGAGC CGGCAGCCCG CAGTGGAGGA GCCAGCGGAG GTCACTGCCA CTGTGCTGGC	180
CAGCAGAGAC GACCACGGAG CCCCTTCTC ATGCCGCACA GAACTGGACA TGCAGCCCCA	240
GGGGCTGGGA CTGTTCGTGA ACACCTCAGC CCCCCGCCAG CTCCGAACCT TT	292

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Asp Arg Val Glu Leu Val Pro Leu Pro Pro Trp Gln Pro Val Gly			
1	5	10	15
Glu Asn Phe Thr Leu Ser Cys Arg Val Pro Gly Ala Gly Pro Arg Ala			
20	25	30	
Ser Leu Thr Leu Thr Leu Leu Arg Gly Gly Gln Glu Leu Ile Arg Arg			
35	40	45	
Ser Phe Val Gly Glu Pro Pro Arg Ala Arg Cys Ala Met Leu Thr Ala			
50	55	60	
Thr Val Leu Ala Arg Arg Glu Asp His Arg Asp Asn Phe Ser Cys Leu			
65	70	75	80
Ala Glu Leu Asp Leu Arg Thr His Gly Leu Gly Leu Phe Ala Asn Ser			
85	90	95	
Ser Ala Pro Arg Gln Leu Arg Thr Phe			
100	105		

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAACTCGAGG CCATGCCTCC ACTTTCC

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCATAAGCTT TATTCCACCG TGACAGGCCAC

30

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AACGTGCGGA GCTGTCTG

18

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACGGAATTCTG AAGCCATCAA CGCCAGG

27

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CATGAATTCC GAATCTTGAG TGGGATG

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATAGAATTCC TCGGGACACC TGTAGCC

27

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CARGGTGACA AGGGCTCG

18

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TATGAATTCA GTTGAGCCAC AGCGAGC

27

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCGGGTCTTA GAGGTGGACA CGCA

24

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGCAGTGTCT CCTGGCTCTG GTTC

24

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGGAAAACCG GGAGACCCGG GAGAACGTGA CCATCTACAG CTTCCCGGCA CCACTCCTGA	60
CCCTGAGCGA ACCCAGCGTC TCCGAGGGGC AGATGGTGAC AGTAACCTGC GCAGCTGGGG	120
CCCAAGCTCT GGTCACACTG GAGGGAGTTC CAGCCGCGGT CCCGGGGCAG CCCGCCAGC	180
TTCAGCTAAA TGCCACCGAG AACGACGACA GACGCAGCTT CTTCTGCGAC GCCACCCTCG	240
ATGTGGACGG GGAGACCCCTG ATCAAGAACAA GGAGCGCAGA GCTTCGTGTC CTATACGCTC	300
CCCCGCTAGA CGATTGGAC TGCCCCAGGA GTTGGACGTG GCCCGAGGGC CCAGAGCAGA	360
CGCTGCGCTG CGAGGCCCGC GGGAAACCCAG AACCCCTCAGT GCACTGTGCG CGCTCCGACG	420
GCGGGGCCGT GCTGGCTCTG GGCCCTGCTGG GTCCAGTCAC TCGGGCGCTC TCAGGCACCTT	480
ACCGCTGCAA GGCGGCCAAT GATCAAGGCG AGGCGGTCAA GGACGTAACG CTAACGGTGG	540
AGTACGCACC AGCGCTGGAC AGCGTGGGCT GCCCAGAACG CATTACTTGG CTGGAGGGAA	600
CAGAAGCCTC GCTGAGCTGT GTGGCGCACG GGGTACCGCC GCCTGATGTG ATCTGCGTGC	660
GCTCTGGAGA ACTCGGGGCC GTCATCGAGG GGCTGTTGCG TGTGGCCCGG GAGCATGCGG	720
GCACCTTACCG CTGCGAAGCC ACCAACCCCTC GGGGCTCTGC GGCCAAAAAT GTGGCCGTCA	780
CGGTGGAATA TGGCCCCAGG TTTGAGGAGC CGAGCTGCC CAGCAATTGG ACATGGGTGG	840
AAGGATCTGG GCGCCTGTTT TCCTGTGAGG TCGATGGAA GCCACAGCCA AGCGTGAAGT	900
GCGTGGGCTC CGGGGGCACC ACTGAGGGGG TGCTGCTGCC GCTGGCACCC CCAGACCTA	960
GTCCCCAGAGC TCCCAGAACAT CCTAGAGTCC TG	992

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCAGCCTCGC GTGGCGTTCG TGGAGCGCGG GGGCTCGCTG TGGCTGAATT GCAGCACCAA	60
CTGCCCTCGG CGGGAGCGCG GTGGCCTGGA GACCTCGCTG CGCCGAAACG GGACCCAGAG	120
GGGTTTGCCTGTTGGCGC GGCAGCTGGT GGACATTGCG GAGCCGGAGA CTCAGCCCGT	180
CTGCTTCTTC CGCTGCGCGC GGCGCACACT ACAGGCGCGT GGGCTCATTG GCACCTTCCA	240

GCGACCAGAT CGCGTAGAGC TGATGCCGCT GCCTCCCTGG CAGCCGGTGG GCGAGAACCTT	300
CACCTGAGC TGTAGGGTCC CCGGCGCCGG GCCCCGTGCG AGCCTCACGC TGACCCCTGCT	360
GCAGGGCGCC CAGGAGCTGA TCCGCCGAG CTTCGCCGGT GAACCACCCC GAGCGCGGGG	420
CGCGGTGCTC ACAGCCACGG TACTGGCTCG GAGGGAGGAC CATGGAGCCA ATTTCTCGTG	480
TCGCGCCGAG CTGGACCTGC GGCCGCACGG ACTGGGACTG TTTGAAAACA GCTCGGCCCC	540
CAGAGAGCTC CGAACCTTCT CCCTGTCTCC GGATGCCCG CGCCTCGCTG CTCCCCGGCT	600
CTTGGAAAGTT GGCTCGGAAA GGCCCGTGAG CTGCACTCTG GACGGACTGT TTCCAGCCTC	660
AGAGGCCAGG GTCTACCTCG CACTGGGGGA CCAGAATCTG AGTCCTGATG TCACCCCTCGA	720
AGGGGACGCA TTCGTGGCCA CTGCCACAGC CACAGCTAGC GCAGAGCAGG AGGGTGCCAG	780
GCAGCTGGTC TGCAACGTCA CCCTGGGGGG CGAAAACCGG GAGACCCGGG AGAACGTGAC	840
CATCTACAGC TTCCCGGCAC CACTCCTGAC CCTGAGCGAA CCCAGCGTCT CCGAGGGGCA	900
GATGGTGACA GTAACCTGCG CAGCTGGGGC CCAAGCTCTG GTCACACTGG AGGGAGTTCC	960
AGCCCGGGTC CCGGGGCAGC CCGCCCAGCT TCAGCTAAAT GCCACCGAGA ACGACGACAG	1020
ACCGAGCTTC TTCTGCGACG CCACCCCTCGA TGTGGACGGG GAGACCCCTGA TCAAGAACAG	1080
GAGCGCAGAG CTTCGTGTCC TATACTGCTCC CCGGCTAGAC GATTCGGACT GCCCCAGGAG	1140
TTGGACGTGG CCCGAGGGCC CAGAGCAGAC GCTGCGCTGC GAGGCCCCGCG GGAACCCAGA	1200
ACCCCTCAGTG CACTGTGCGC GCTCCGACGG CGGGGCCGTG CTGGCTCTGG GCCTGCTGGG	1260
TCCAGTCACT CGGGCGCTCT CAGGCACCTTA CCGCTGCAAG GCAGGCCAATG ATCAAGGCAG	1320
GGCGGTCAAG GACGTAACGC TAACGGTGGA GTACGCACCA GCGCTGGACA GCGTGGGCTG	1380
CCCAGAACGC ATTACTTGGC TGGAGGGAAC AGAACGCTCG CTGAGCTGTG TGGCGCACGG	1440
GGTACCGCCG CCTGATGTGA TCTGCGTGC CTCTGGAGAA CTGGGGCCCG TCATCGAGGG	1500
GCTGTTGCGT GTGGCCCGGG AGCATGCGGG CACTTACCGC TGCAGAGCCA CCAACCCCTCG	1560
GGGCTCTGCG GCCAAAAATG TGGCCGTCAC GGTGGAATAT GGCCCCAGGT TTGAGGAGCC	1620
GAGCTGCCCG AGCAATTGGA CATGGGTGGA AGGATCTGGG CGCCTGTTTT CCTGTGAGGT	1680
CGATGGGAAG CCACAGCCAA GCGTGAAGTG CGTGGGCTCC GGGGGCACCA CTGAGGGGGT	1740
GCTGCTGCCG CTGGCACCCC CAGACCCTAG TCCCAGAGCT CCCAGAACCTC CTAGAGTCCT	1800
GGCACCCGGT ATCTACGTCT GCAACGCCAC CAACCGCCAC GGCTCCGTGG CCAAAACAGT	1860
CGTCGTGAGC GCGGAGTCGC CACCGGAGAT GGATGAATCT ACCTGCCCAA GTCACCGAGAC	1920
GTGGCTGGAA GGGGCTGAGG CTTCCGCGCT GGCGTGCCT GCGCCGGGTC GCGCTTCCCC	1980
AGGAGTGCAGC TGCTCTCGGG AAGGCATCCC ATGGCCTGAG CAGCAGCGCG TGTCCCCAGA	2040
GGACCGGGGC ACTTACCACT GTGTGGCCAC CAATGCGCAT GGCACGGACT CCCGGACCCT	2100
CACTGTGGGC GTGGAATACC GGCGAGTGGT GGCGAACCTT GCTGCCCTCGC CCCCTGGAGG	2160

CGTGCGCCCA GGAGGAAACT TCACGTTGAC CTGCCGCGCG GAGGCCTGGC CTCCAGCCC	2220
GATCAGCTGG CGCGCGCCCC CGAGGGCCCT CAACATCGC CTGTCGAGCA ACAACAGCAC	2280
ACTGAGCGTG GCAGGCGCCA TGGGAAGCCA CGGCGGCGAG TACGAGTGC CACGCACCAA	2340
CGCGCACGGG CGCCACCGCGC GGCGCATCAC GGTGCGCGTG GCCGGTCCGT GGCTATGGGT	2400
CGCCGTGGC GGCGCGCGG GGGCGCGGC GCTGCTGGCC GCGGGGGCG GCCTGCCCT	2460
CTACGTGCAG TCCACCGCCT GCAAGAAGGG CGAGTACAAC GTGCAGGAGG CCGAGAGCTC	2520
AGGCGAGGCC GTGTGCTGA ACGGAGCGGG CGGCAGCGCT GGCAGGGCGG CAGGCGCGGA	2580
GGCGGACCC GAGGCGCGG GGGCGCGGC CGAGTCGCCG GCGGAGGGCG AGGTCTTCGC	2640
CATACAGCTG ACATCGCGT GAGCCCGCTC CCCTCTCCGC GGGCCGGGAC GCCCCCCAGA	2700
CTCACACGGG GGCTTATTAA TTGCTTTATT TATTTACTTA TTCATTATTATT TATGTATTCA	2760
ACTCCAAGGG AATTC	2775

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1557 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGCGCTCTCC TCGCCTCTG TGCTTCCCC GCGCGGCCA TGCCAGGGCC TTCGCCAGGG	60
CTGCGCCGGG CGCTACTCGG CCTCTGGGCT GCTCTGGCC TGGGGCTCTT CGGCCTCTCA	120
GCGGTCTCGC AGGAGCCCTT CTGGCGGGAC CTGCAGCCTC GCGTGGCGTT CGTGGAGCGC	180
GGGGGCTCGC TGTGGCTGAA TTGCAGCACC AACTGCCCTC GGCCGGAGCG CGGTGGCCTG	240
GAGACCTCGC TGCGCCAAA CGGGACCCAG AGGGGTTTGC GTTGGTTGGC GCGGCAGCTG	300
GTGGACATTC GCGAGCCGGA GACTCAGCCC GTCTGCTTCT TCCGCTGCC GCGGCACACA	360
CTACAGGCGC GTGGGCTCAT TCGCACTTTTC CAGCGACCAG ATCGCGTAGA GCTGATGCCG	420
CTGCCTCCCT GGCAGCCGGT GGGCGAGAAC TTCACCCCTGA GCTGTAGGGT CCCCAGCGCC	480
GGGCCCGTG CGAGCCTCAC GCTGACCTG CTGCGGGCG CCCAGGAGCT GATCCGCCGC	540
AGCTCGCCG GTGAACCACC CCGAGCGCGG GGCGCGGTGC TCACAGCCAC GGTACTGGCT	600
CGGAGGGAGG ACCATGGAGC CAATTCTCG TGTCGCGCC AGCTGGACCT GCGGCCGCAC	660
GGACTGGAC TGTTGAAAA CAGCTCGGCC CCCAGAGAGC TCCGAACCTT CTCCCTGTCT	720
CGGGATGCCG CGCGCCTCGC TGCTCCCCGG CTCTTGAAG TTGGCTCGGA AAGGCGCGTG	780
AGCTGCACTC TGGACGGACT GTTTCCAGCC TCAGAGGCCA GGGTCTACCT CGCACTGGGG	840
GACCAGAATC TGAGTCCTGA TGTCAACCTC GAAGGGGACG CATTGCGGCC CACTGCCACA	900

GCCACAGCTA GCGCAGAGCA GGAGGGTGCC AGGCAGCTGG TCTGCAACGT CACCCTGGGG	960
GGCGAAAACC GGGAGACCCG GGAGAACGTG ACCATCTACA GCTTCCCGGC ACCACTCCTG	1020
ACCTCTGAGCG AACCCAGCGT CTCCGAGGGG CAGATGGTGA CAGTAACCTG CGCAGCTGGG	1080
GCCCAAGCTC TGGTCACACT GGAGGGAGTT CCAGCCGCGG TCCCAGGGCA GCCCGCCCAG	1140
CTTCAGCTAA ATGCCACCGA GAACGACGAC AGACGCAGCT TCTTCTGCGA CGCCACCCCTC	1200
GATGTGGACG GGGAGACCCCT GATCAAGAAC AGGAGCGCAG AGCTTCGTGT CCTATACGCT	1260
CCCCGGCTAG ACGATTCGGA CTGCCCCAGG AGTTGGACGT GGCCCGAGGG CCCAGAGCAG	1320
ACGCTGCGCT GCGAGGCCCG CGGGAAACCCA GAACCCCTCAG TGCACTGTGC GCGCTCCGAC	1380
GGCGGGGCCG TGCTGGCTCT GGGCCTGCTG GGTCCAGTCA CTCGGCGCT CTCAGGCCT	1440
TACCGCTGCA AGGCAGCCAA TGATCAAGGC GAGGCAGTCA AGGACGTAAC GCTAACGGTG	1500
GAGTACGCAC CAGCGCTGGA CAGCGTGGGC TGCCAGAAC GCATTACTTG GCTGGAG	1557

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 40..2814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CGCGCTCTCC TCGCCTCCTG TGCTTTCCCC GCGCGGGCG ATG CCA GGG CCT TCG Met Pro Gly Pro Ser 1 5	54
CCA GGG CTG CGC CGG GCG CTA CTC GGC CTC TGG GCT GCT CTG GGC CTG Pro Gly Leu Arg Arg Ala Leu Leu Gly Leu Trp Ala Ala Leu Gly Leu 10 15 20	102
GGG CTC TTC GGC CTC TCA GCG GTC TCG CAG GAG CCC TTC TGG GCG GAC Gly Leu Phe Gly Leu Ser Ala Val Ser Gln Glu Pro Phe Trp Ala Asp 25 30 35	150
CTG CAG CCT CGC GTG GCG TTC GTG GAG CGC GGG GGC TCG CTG TGG CTG Leu Gln Pro Arg Val Ala Phe Val Glu Arg Gly Ser Leu Trp Leu 40 45 50	198
AAT TGC AGC ACC AAC TGC CCT CGG CCG GAG CGC GGT GGC CTG GAG ACC Asn Cys Ser Thr Asn Cys Pro Arg Pro Glu Arg Gly Gly Leu Glu Thr 55 60 65	246
TCG CTG CGC CGA AAC GGG ACC CAG AGG GGT TTG CGT TGG TTG GCG CGG Ser Leu Arg Arg Asn Gly Thr Gln Arg Gly Leu Arg Trp Leu Ala Arg 70 75 80 85	294

CAG CTG GTG GAC ATT CGC GAG CCG GAG ACT CAG CCC GTC TGC TTC TTC Gln Leu Val Asp Ile Arg Glu Pro Glu Thr Gln Pro Val Cys Phe Phe 90 95 100	342
CGC TGC GCG CGG CGC ACA CTA CAG GCG CGT GGG CTC ATT CGC ACT TTC Arg Cys Ala Arg Arg Thr Leu Gln Ala Arg Gly Leu Ile Arg Thr Phe 105 110 115	390
CAG CGA CCA GAT CGC GTA GAG CTG ATG CCG CTG CCT CCC TGG CAG CCG Gln Arg Pro Asp Arg Val Glu Leu Met Pro Leu Pro Pro Trp Gln Pro 120 125 130	438
GTG GGC GAG AAC TTC ACC CTG AGC TGT AGG GTC CCC GGC GCC GGG CCC Val Gly Glu Asn Phe Thr Leu Ser Cys Arg Val Pro Gly Ala Gly Pro 135 140 145	486
CGT GCG AGC CTC ACG CTG ACC CTG CTG CGG GGC GCC CAG GAG CTG ATC Arg Ala Ser Leu Thr Leu Thr Leu Arg Gly Ala Gln Glu Leu Ile 150 155 160 165	534
CGC CGC AGC TTC GCC GGT GAA CCA CCC CGA GCG CGG GGC GCG GTG CTC Arg Arg Ser Phe Ala Gly Glu Pro Pro Arg Ala Arg Gly Ala Val Leu 170 175 180	582
ACA GCC ACG GTA CTG GCT CGG AGG GAG GAC CAT GGA GCC AAT TTC TCG Thr Ala Thr Val Leu Ala Arg Arg Glu Asp His Gly Ala Asn Phe Ser 185 190 195	630
TGT CGC GCC GAG CTG GAC CTG CGG CCG CAC GGA CTG GGA CTG TTT GAA Cys Arg Ala Glu Leu Asp Leu Arg Pro His Gly Leu Gly Leu Phe Glu 200 205 210	678
AAC AGC TCG GCC CCC AGA GAG CTC CGA ACC TTC TCC CTG TCT CCG GAT Asn Ser Ser Ala Pro Arg Glu Leu Arg Thr Phe Ser Leu Ser Pro Asp 215 220 225	726
GCC CCG CGC CTC GCT CCC CGG CTC TTG GAA GTT GGC TCG GAA AGG Ala Pro Arg Leu Ala Ala Pro Arg Leu Leu Glu Val Gly Ser Glu Arg 230 235 240 245	774
CCC GTG AGC TGC ACT CTG GAC GGA CTG TTT CCA GCC TCA GAG GCC AGG Pro Val Ser Cys Thr Leu Asp Gly Leu Phe Pro Ala Ser Glu Ala Arg 250 255 260	822
GTC TAC CTC GCA CTG GGG GAC CAG AAT CTG AGT CCT GAT GTC ACC CTC Val Tyr Leu Ala Leu Gly Asp Gln Asn Leu Ser Pro Asp Val Thr Leu 265 270 275	870
GAA GGG GAC GCA TTC GTG GCC ACT GCC ACA GCA GCA GCT AGC GCA GAG Glu Gly Asp Ala Phe Val Ala Thr Ala Thr Ala Ser Ala Glu 280 285 290	918
CAG GAG GGT GCC AGG CAG CTG GTC AAC GTC ACC CTG GGG GGC GAA Gln Glu Gly Ala Arg Gln Leu Val Cys Asn Val Thr Leu Gly Gly Glu 295 300 305	966
AAC CGG GAG ACC CGG GAG AAC GTG ACC ATC TAC AGC TTC CCG GCA CCA Asn Arg Glu Thr Arg Glu Asn Val Thr Ile Tyr Ser Phe Pro Ala Pro 310 315 320 325	1014
CTC CTG ACC CTG AGC GAA CCC AGC GTC TCC GAG GGG CAG ATG GTG ACA Leu Leu Thr Leu Ser Glu Pro Ser Val Ser Glu Gly Gln Met Val Thr 330 335 340	1062

GTA ACC TGC GCA GCT GGG GCC CAA GCT CTG GTC ACA CTG GAG GGA GTT Val Thr Cys Ala Ala Gly Ala Gln Ala Leu Val Thr Leu Glu Gly Val 345 350 355	1110
CCA GCC GCG GTC CCG GGG CAG CCC GCC CAG CTT CAG CTA AAT GCC ACC Pro Ala Ala Val Pro Gly Gln Pro Ala Gln Leu Gln Leu Asn Ala Thr 360 365 370	1158
GAG AAC GAC GAC AGA CGC AGC TTC TTC TGC GAC GCC ACC CTC GAT GTG Glu Asn Asp Asp Arg Arg Ser Phe Phe Cys Asp Ala Thr Leu Asp Val 375 380 385	1206
GAC GGG GAG ACC CTG ATC AAG AAC AGG AGC GCA GAG CTT CGT GTC CTA Asp Gly Glu Thr Leu Ile Lys Asn Arg Ser Ala Glu Leu Arg Val Leu 390 395 400 405	1254
TAC GCT CCC CGG CTA GAC GAT TCG GAC TGC CCC AGG AGT TGG ACG TGG Tyr Ala Pro Arg Leu Asp Asp Ser Asp Cys Pro Arg Ser Trp Thr Trp 410 415 420	1302
CCC GAG GGC CCA GAG CAG ACG CTG CGC TGC GAG GCC CGC GGG AAC CCA Pro Glu Gly Pro Glu Gln Thr Leu Arg Cys Glu Ala Arg Gly Asn Pro 425 430 435	1350
GAA CCC TCA GTG CAC TGT GCG CGC TCC GAC GGC GGG GCC GTG CTG GCT Glu Pro Ser Val His Cys Ala Arg Ser Asp Gly Gly Ala Val Leu Ala 440 445 450	1398
CTG GGC CTG CTG GGT CCA GTC ACT CGG GCG CTC TCA GGC ACT TAC CGC Leu Gly Leu Leu Gly Pro Val Thr Arg Ala Leu Ser Gly Thr Tyr Arg 455 460 465	1446
TGC AAG GCG GCC AAT GAT CAA GGC GAG GCG GTC AAG GAC GTA ACG CTA Cys Lys Ala Ala Asn Asp Gln Gly Glu Ala Val Lys Asp Val Thr Leu 470 475 480 485	1494
ACG GTG GAG TAC GCA CCA GCG CTG GAC AGC GTG GGC TGC CCA GAA CGC Thr Val Glu Tyr Ala Pro Ala Leu Asp Ser Val Gly Cys Pro Glu Arg 490 495 500	1542
ATT ACT TGG CTG GAG GGA ACA GAA GCC TCG CTG AGC TGT GTG GCG CAC Ile Thr Trp Leu Glu Gly Thr Glu Ala Ser Leu Ser Cys Val Ala His 505 510 515	1590
GGG GTA CCG CCG CCT GAT GTG ATC TGC GTG CGC TCT GGA GAA CTC GGG Gly Val Pro Pro Pro Asp Val Ile Cys Val Arg Ser Gly Glu Leu Gly 520 525 530	1638
GCC GTC ATC GAG GGG CTG TTG CGT GTG GCC CGG GAG CAT GCG GGC ACT Ala Val Ile Glu Gly Leu Leu Arg Val Ala Arg Glu His Ala Gly Thr 535 540 545	1686
TAC CGC TGC GAA GCC ACC AAC CCT CGG GGC TCT GCG GCC AAA AAT GTG Tyr Arg Cys Glu Ala Thr Asn Pro Arg Gly Ser Ala Ala Lys Asn Val 550 555 560 565	1734
GCC GTC ACG GTG GAA TAT GGC CCC AGG TTT GAG GAG CCG AGC TGC CCC Ala Val Thr Val Glu Tyr Pro Arg Phe Glu Glu Pro Ser Cys Pro 570 575 580	1782
AGC AAT TGG ACA TGG GTG GAA GGA TCT GGG CGC CTG TTT TCC TGT GAG Ser Asn Trp Thr Trp Val Glu Gly Ser Gly Arg Leu Phe Ser Cys Glu 585 590 595	1830

GTC GAT GGG AAG CCA CAG CCA AGC GTG AAG TGC GTG GGC TCC GGG GGC Val Asp Gly Lys Pro Gln Pro Ser Val Lys Cys Val Gly Ser Gly Gly 600 605 610	1878
ACC ACT GAG GGG GTG CTG CTG CCG CTG GCA CCC CCA GAC CCT AGT CCC Thr Thr Glu Gly Val Leu Leu Pro Leu Ala Pro Pro Asp Pro Ser Pro 615 620 625	1926
AGA GCT CCC AGA ATC CCT AGA GTC CTG GCA CCC GGT ATC TAC GTC TGC Arg Ala Pro Arg Ile Pro Arg Val Leu Ala Pro Gly Ile Tyr Val Cys 630 635 640 645	1974
AAC GCC ACC AAC CGC CAC GGC TCC GTG GCC AAA ACA GTC GTC GTG AGC Asn Ala Thr Asn Arg His Gly Ser Val Ala Lys Thr Val Val Val Ser 650 655 660	2022
GCG GAG TCG CCA CCG GAG ATG GAT GAA TCT ACC TGC CCA AGT CAC CAG Ala Glu Ser Pro Pro Glu Met Asp Glu Ser Thr Cys Pro Ser His Gln 665 670 675	2070
ACG TGG CTG GAA GGG GCT GAG GCT TCC GCG CTG GCC TGC GCC GCC CGG Thr Trp Leu Glu Gly Ala Glu Ala Ser Ala Leu Ala Cys Ala Ala Arg 680 685 690	2118
GGT CGC CCT TCC CCA GGA GTG CGC TGC TCT CGG GAA GGC ATC CCA TGG Gly Arg Pro Ser Pro Gly Val Arg Cys Ser Arg Glu Gly Ile Pro Trp 695 700 705	2166
CCT GAG CAG CAG CGC GTG TCC CGA GAG GAC GCG GGC ACT TAC CAC TGT Pro Glu Gln Gln Arg Val Ser Arg Glu Asp Ala Gly Thr Tyr His Cys 710 715 720 725	2214
GTG GCC ACC AAT GCG CAT GGC ACG GAC TCC CGG ACC GTC ACT GTG GGC Val Ala Thr Asn Ala His Gly Thr Asp Ser Arg Thr Val Thr Val Gly 730 735 740	2262
GTG GAA TAC CGG CCA GTG GTG GCC GAA CTT GCT GCC TCG CCC CCT GGA Val Glu Tyr Arg Pro Val Val Ala Glu Leu Ala Ala Ser Pro Pro Gly 745 750 755	2310
GGC GTG CGC CCA GGA GGA AAC TTC ACG TTG ACC TGC CGC GCG GAG GCC Gly Val Arg Pro Gly Gly Asn Phe Thr Leu Thr Cys Arg Ala Glu Ala 760 765 770	2358
TGG CCT CCA GCC CAG ATC ACG TGG CGC GCG CCC CCG AGG GCC CTC AAC Trp Pro Pro Ala Gln Ile Ser Trp Arg Ala Pro Pro Arg Ala Leu Asn 775 780 785	2406
ATC GGC CTG TCG AGC AAC AAC AGC ACA CTG AGC GTG GCA GGC GCC ATG Ile Gly Leu Ser Ser Asn Asn Ser Thr Leu Ser Val Ala Gly Ala Met 790 795 800 805	2454
GGA AGC CAC GGC GGC GAG TAC GAG TGC GCA CGC ACC AAC GCG CAC GGG Gly Ser His Gly Gly Glu Tyr Glu Cys Ala Arg Thr Asn Ala His Gly 810 815 820	2502
CGC CAC GCG CGG CGC ATC ACG GTG CGC GTG GCC GGT CCG TGG CTA TGG Arg His Ala Arg Arg Ile Thr Val Arg Val Ala Gly Pro Trp Leu Trp 825 830 835	2550
GTC GCC GTG GGC GGC GCG GCG GGG GGC GCG GCG CTG CTG GCC GCG GGG Val Ala Val Gly Gly Ala Ala Gly Gly Ala Ala Leu Leu Ala Ala Gly 840 845 850	2598

GCC GGC CTG GCC TTC TAC GTG CAG TCC ACC GCC TGC AAG AAG GGC GAG Ala Gly Leu Ala Phe Tyr Val Gln Ser Thr Ala Cys Lys Lys Gly Glu 855 860 865	2646
TAC AAC GTG CAG GAG GCC GAG AGC TCA GGC GAG GCC GTG TGT CTG AAC Tyr Asn Val Gln Glu Ala Glu Ser Ser Gly Glu Ala Val Cys Leu Asn 870 875 880 885	2694
GGA GCG GGC GGC GCT GGC GGG GCG GCA GGC GCG GAG GGC GGA CCC Gly Ala Gly Gly Ala Gly Ala Ala Gly Ala Glu Gly Gly Pro 890 895 900	2742
GAG GCG GCG GGG GGC GCG GCC GAG TCG CCG GCG GAG GGC GAG GTC TTC Glu Ala Ala Gly Ala Ala Glu Ser Pro Ala Glu Gly Glu Val Phe 905 910 915	2790
GCC ATA CAG CTG ACA TCG GCG TGAGCCCCGCT CCCCTCTCCG CGGGCCGGGA Ala Ile Gln Leu Thr Ser Ala 920 925	2841
CGCCCCCCCAG ACTCACACGG GGGCTTATTT ATTGCTTTAT TTATTTACTT ATTCAATTAT	2901
TTATGTATTC AACTCCAAGG GAATTC	2927

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 924 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Pro Gly Pro Ser Pro Gly Leu Arg Arg Ala Leu Leu Gly Leu Trp 1 5 10 15
Ala Ala Leu Gly Leu Gly Leu Phe Gly Leu Ser Ala Val Ser Gln Glu 20 25 30
Pro Phe Trp Ala Asp Leu Gln Pro Arg Val Ala Phe Val Glu Arg Gly 35 40 45
Gly Ser Leu Trp Leu Asn Cys Ser Thr Asn Cys Pro Arg Pro Glu Arg 50 55 60
Gly Gly Leu Glu Thr Ser Leu Arg Arg Asn Gly Thr Gln Arg Gly Leu 65 70 75 80
Arg Trp Leu Ala Arg Gln Leu Val Asp Ile Arg Glu Pro Glu Thr Gln 85 90 95
Pro Val Cys Phe Phe Arg Cys Ala Arg Arg Thr Leu Gln Ala Arg Gly 100 105 110
Leu Ile Arg Thr Phe Gln Arg Pro Asp Arg Val Glu Leu Met Pro Leu 115 120 125
Pro Pro Trp Gln Pro Val Gly Glu Asn Phe Thr Leu Ser Cys Arg Val 130 135 140

Pro Gly Ala Gly Pro Arg Ala Ser Leu Thr Leu Thr Leu Leu Arg Gly
145 150 155 160

Ala Gln Glu Leu Ile Arg Arg Ser Phe Ala Gly Glu Pro Pro Arg Ala
165 170 175

Arg Gly Ala Val Leu Thr Ala Thr Val Leu Ala Arg Arg Glu Asp His
180 185 190

Gly Ala Asn Phe Ser Cys Arg Ala Glu Leu Asp Leu Arg Pro His Gly
195 200 205

Leu Gly Leu Phe Glu Asn Ser Ser Ala Pro Arg Glu Leu Arg Thr Phe
210 215 220

Ser Leu Ser Pro Asp Ala Pro Arg Leu Ala Ala Pro Arg Leu Leu Glu
225 230 235 240

Val Gly Ser Glu Arg Pro Val Ser Cys Thr Leu Asp Gly Leu Phe Pro
245 250 255

Ala Ser Glu Ala Arg Val Tyr Leu Ala Leu Gly Asp Gln Asn Leu Ser
260 265 270

Pro Asp Val Thr Leu Glu Gly Asp Ala Phe Val Ala Thr Ala Thr Ala
275 280 285

Thr Ala Ser Ala Glu Gln Glu Gly Ala Arg Gln Leu Val Cys Asn Val
290 295 300

Thr Leu Gly Gly Glu Asn Arg Glu Thr Arg Glu Asn Val Thr Ile Tyr
305 310 315 320

Ser Phe Pro Ala Pro Leu Leu Thr Leu Ser Glu Pro Ser Val Ser Glu
325 330 335

Gly Gln Met Val Thr Val Thr Cys Ala Ala Gly Ala Gln Ala Leu Val
340 345 350

Thr Leu Glu Gly Val Pro Ala Ala Val Pro Gly Gln Pro Ala Gln Leu
355 360 365

Gln Leu Asn Ala Thr Glu Asn Asp Asp Arg Arg Ser Phe Phe Cys Asp
370 375 380

Ala Thr Leu Asp Val Asp Gly Glu Thr Leu Ile Lys Asn Arg Ser Ala
385 390 395 400

Glu Leu Arg Val Leu Tyr Ala Pro Arg Leu Asp Asp Ser Asp Cys Pro
405 410 415

Arg Ser Trp Thr Trp Pro Glu Gly Pro Glu Gln Thr Leu Arg Cys Glu
420 425 430

Ala Arg Gly Asn Pro Glu Pro Ser Val His Cys Ala Arg Ser Asp Gly
435 440 445

Gly Ala Val Leu Ala Leu Gly Leu Leu Gly Pro Val Thr Arg Ala Leu
450 455 460

Ser Gly Thr Tyr Arg Cys Lys Ala Ala Asn Asp Gln Gly Glu Ala Val
465 470 475 480

Lys Asp Val Thr Leu Thr Val Glu Tyr Ala Pro Ala Leu Asp Ser Val
485 490 495

Gly Cys Pro Glu Arg Ile Thr Trp Leu Glu Gly Thr Glu Ala Ser Leu
500 505 510

Ser Cys Val Ala His Gly Val Pro Pro Pro Asp Val Ile Cys Val Arg
515 520 525

Ser Gly Glu Leu Gly Ala Val Ile Glu Gly Leu Leu Arg Val Ala Arg
530 535 540

Glu His Ala Gly Thr Tyr Arg Cys Glu Ala Thr Asn Pro Arg Gly Ser
545 550 555 560

Ala Ala Lys Asn Val Ala Val Thr Val Glu Tyr Gly Pro Arg Phe Glu
565 570 575

Glu Pro Ser Cys Pro Ser Asn Trp Thr Trp Val Glu Gly Ser Gly Arg
580 585 590

Leu Phe Ser Cys Glu Val Asp Gly Lys Pro Gln Pro Ser Val Lys Cys
595 600 605

Val Gly Ser Gly Gly Thr Thr Glu Gly Val Leu Leu Pro Leu Ala Pro
610 615 620

Pro Asp Pro Ser Pro Arg Ala Pro Arg Ile Pro Arg Val Leu Ala Pro
625 630 635 640

Gly Ile Tyr Val Cys Asn Ala Thr Asn Arg His Gly Ser Val Ala Lys
645 650 655

Thr Val Val Val Ser Ala Glu Ser Pro Pro Glu Met Asp Glu Ser Thr
660 665 670

Cys Pro Ser His Gln Thr Trp Leu Glu Gly Ala Glu Ala Ser Ala Leu
675 680 685

Ala Cys Ala Ala Arg Gly Arg Pro Ser Pro Gly Val Arg Cys Ser Arg
690 695 700

Glu Gly Ile Pro Trp Pro Glu Gln Gln Arg Val Ser Arg Glu Asp Ala
705 710 715 720

Gly Thr Tyr His Cys Val Ala Thr Asn Ala His Gly Thr Asp Ser Arg
725 730 735

Thr Val Thr Val Gly Val Glu Tyr Arg Pro Val Val Ala Glu Leu Ala
740 745 750

Ala Ser Pro Pro Gly Gly Val Arg Pro Gly Gly Asn Phe Thr Leu Thr
755 760 765

Cys Arg Ala Glu Ala Trp Pro Pro Ala Gln Ile Ser Trp Arg Ala Pro
770 775 780

Pro Arg Ala Leu Asn Ile Gly Leu Ser Ser Asn Asn Ser Thr Leu Ser
785 790 795 800

Val Ala Gly Ala Met Gly Ser His Gly Gly Glu Tyr Glu Cys Ala Arg
805 810 815

- 90 -

Thr Asn Ala His Gly Arg His Ala Arg Arg Ile Thr Val Arg Val Ala
820 825 830

Gly Pro Trp Leu Trp Val Ala Val Gly Gly Ala Ala Gly Gly Ala Ala
835 840 845

Leu Leu Ala Ala Gly Ala Gly Leu Ala Phe Tyr Val Gln Ser Thr Ala
850 855 860

Cys Lys Lys Gly Glu Tyr Asn Val Gln Glu Ala Glu Ser Ser Gly Glu
865 870 875 880

Ala Val Cys Leu Asn Gly Ala Gly Gly Ala Gly Gly Ala Ala Gly
885 890 895

Ala Glu Gly Gly Pro Glu Ala Ala Gly Gly Ala Ala Glu Ser Pro Ala
900 905 910

Glu Gly Glu Val Phe Ala Ile Gln Leu Thr Ser Ala
915 920

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTACTTACAG GATCCGCGGT CTCGCAGGAG CCCTTCTGGG CGGACCTACA GCCTGCGTGG 60

CGTTC 65

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATTTCTCTCG AGGATGGTCA CGTTCTCCCCG G 31

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATTTCTGGAT CCTACAGCTT CCCGGCACCA CTC 33

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATTTCTCTCG AGTTCCACGC CCACAGTGAC GG 32

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1687 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGATCCTTTG AGCCCTGAAA GTCGAGGTTG CAGTGAGCCT TGATCGTGCC ACTGCACTCC	60
AGCCTGGGG ACAGAGCACG ACCCTGTCTC CAAAAATAAA ATAAAAATAA AAATAAATAT	120
TGGCGGGGA ACCCTCTGGA ATCAATAAAG GCTTCCTTAA CCAGCCTCTG TCCTGTGACC	180
TAAGGGTCCG CATTACTGCC CTTCTCGGA GGAACTGGTT TGTTTTGTT GTTGTGTTG	240
TTTTGCGAT CACTTCTCC AAGTTCTTG TCTCCCTGAG GGCACCTGAG GTTCCCTCAC	300
TCAGGGCCA CCTGGGTCC CGAACCCCCA GACTCTGTGT ATCCCCAGCG GGTGTCACAG	360
AAACCTCTCC TTCTGCTGGC CTTATCGAGT GGGATCAGCG CGGCCGGGA GAGCCACGGG	420
CAGGGCGGG GTGGGGTTCA TGGTATGGCT TTCCTGATTG GCGCCGCCGC CACCACCGG	480
CAGCTCTGAT TGGATGTTAA GTTCCCTATC CCAGCCCCAC CTTCAGACCC TGTGCTTCC	540
TGGAGGCCAA ACAACTGTGG AGCGAGAACT CATCTCCAAA ATAACCTTACC ACGCTGGAGT	600
GAGACCACGA ATGGTGGGA GGGGAGGGTC CCACGGACAT ATTGAGGGAC GTGGATACGC	660
AGAAGAGGTA TCCATGTGGT GGCAGCCGGG AAGGGGTGAT CAGATGGTCC ACAGGGAATA	720
TCACAAACTC GAATTCTGAC GATGTTCTGG TAGTCACCCA GCCAGATGAG CGCATGGAGT	780
TGGCGGTGGG GGGTGTCAA GCTTGGGCC CGGAAGCGGA GTCAAAAGCA TCACCCCTCGG	840
TCCCTTGTTC TCGCGTGGAT GTCAGGGCCT CCACCCACCG AGCAGAAGGC GGACTCAGGG	900
GCGCTCCAGG GTGGCTCGAG CTCACACACG CTGAGTAGAC ACGTGCCTGC TGCACCCCTGG	960
GTAAATACAG ACCCGGAGCC GAGCGGATTC TAATTTAGAC GCCCGCGAAC GCTGCGCGCA	1020
CGCACACGTG TCCTCGGCTC GCTGGCACTT TCGTCCCCTGCC CCCTCCGTGCGT CGTGCCTGGAG	1080

CTGACCCGGA GGGGTGCTTA GAGGTATGGC TCCGCGGGGT CAAAAGGAGA AGGATCAGTG	1140
AGAGAGGATC CCCACACCCT CCCCTAGAAC TGTCCTTCC CCATCCAGTG CCTCCCAAAT	1200
CTCTCTTAGT CCCCAAATGT ATCCCCGCC TAAGGGCGC TGTTGGGAGG AGCTAAATGT	1260
GGGGGCGGAG CTCGGAGTCC AGCTTATTAT CATGGCATCT CAGCCAGGGC TGGGGTAGGG	1320
GTTTGGGAAG GGCAACCCAG CATCCCCGA TCCCAGAGTC GCGGCCGGGG ATGACGCGAG	1380
AGAGCGTGGT CGCCCCCAGA AGGCCCTGGG CCATCATGCC GGCCCTCCACG TAGACCCAG	1440
GGGTCGCTCA CTCCCTGCCAG CTCGCCTTCA CCAAGGCCAG GAGCTTAGCG CACGCTCGCC	1500
TCCCGCCCCC CCGCCGCCCTC TGCCGCCGCC CCCTCCTTGG AAACCAAGTT ACCAACGTTA	1560
AACCAATCCC CAAGCGAAC TCTGTCTCCC CCACACCCCA CCCGCCGCC CGCGCGGAGC	1620
CGTCCTCTAG CCCAGCTCCT CGGCTCGCGC TCTCCTCGCC TCCTGTGCTT TCCCCGCCGC	1680
GGCGATG	1687

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAGAACTAAG CTTACAGGAG GCGAGGAGAG CGCGAG	36
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(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CAACAATGCT AGCCAAGCGC AACTCTGTCT C	31
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(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAACAATGCT AGCCTTGGAA ACCAAGTTAC C	31
------------------------------------	----

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAACAATGCT AGCAGGAGCT TAGCGCACGC TCG

33

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CAACAATGCT AGCCATGCCG GCCTCCACGT AG

32

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CAACAATGCT AGCGTCAGC TTATTATCAT G

31

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CAACAATGCT AGCCTTAGTC CCCAAATGTA TC

32

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CAACAATGCT AGCGGAGAAG GATCAGTGAG

30

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CAACAATGCT AGCCTCCACC CACCGAGCAG AAG

33